

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 12:30:12 ; Search time 0.001 Seconds

(without alignments)
63.400 Million cell updates/sec

Title: US-10-003-919-21

Perfect score: 20
Sequence: 1 ATGGACTCGTCGACGCAC 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 132 seqs, 1585 residues

Total number of hits satisfying chosen parameters: 264

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 132 summaries

Database : rnpdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	1	US-10-003-919-21
2	12.2	61.0	17	1	US-10-712-672-48
3	11.8	59.0	18	1	US-09-790-264-28
4	11.8	59.0	18	1	US-10-269-353-28
5	11.4	57.0	17	1	US-10-138-674-7618
6	11.4	57.0	17	1	US-10-138-674-7619
7	11.4	57.0	17	1	US-10-287-949A-7618
8	11.4	57.0	17	1	US-10-287-949A-7619
9	11.4	57.0	17	1	US-10-712-672-619
10	11.2	56.0	17	1	US-09-866-108-9914
11	11.2	56.0	17	1	US-09-866-108-9915
12	11.2	56.0	17	1	US-10-712-672-618
13	10.8	54.0	16	1	US-10-712-672-1569
14	10.4	52.0	15	1	US-10-312-273-661
15	10.4	52.0	15	1	US-09-848-754A-9285
16	10.4	52.0	15	1	US-10-160-388-9
17	10.4	52.0	16	1	US-10-435-696-232
18	10.4	52.0	16	1	US-10-138-674-5820
19	10.4	52.0	16	1	US-10-287-949A-5820
20	10.2	51.0	15	1	US-09-825-805-143
21	10.2	51.0	15	1	US-09-740-332-4783
22	10.2	51.0	15	1	US-09-817-879-4783
23	10.2	51.0	15	1	US-10-339-674-740
24	10.2	51.0	15	1	US-10-339-674-1891
25	10	50.0	12	1	US-10-096-718-9
26	10	50.0	12	1	US-10-096-718-29
27	10	50.0	12	1	US-10-347-510A-105
28	10	50.0	15	1	US-09-544-934B-105
29	9.8	49.0	15	1	US-10-189-356-30
30	9.8	49.0	15	1	US-10-138-674-4143
31	9.8	49.0	15	1	US-10-287-949A-4143
32	9.4	47.0	14	1	US-10-231-230-34
33	9.4	47.0	14	1	US-10-231-249-34

34	9.4	47.0	14	1	US-10-084-839-3847	Sequence 3847, Ap
35	9	45.0	10	1	US-10-033-145-833	Sequence 833, App
36	9	45.0	10	1	US-10-033-145-1372	Sequence 1372, Ap
37	9	45.0	10	1	US-10-330-627-1189	Sequence 1189, Ap
38	9	45.0	13	1	US-09-238-351-45	Sequence 45, Appl
39	9	45.0	13	1	US-09-238-351-47	Sequence 47, Appl
40	9	45.0	13	1	US-09-238-351-51	Sequence 51, Appl
41	9	45.0	13	1	US-09-238-351-53	Sequence 53, Appl
42	9	45.0	13	1	US-09-238-351-59	Sequence 59, Appl
43	9	45.0	13	1	US-09-238-351-61	Sequence 61, Appl
44	9	45.0	13	1	US-09-510-378-23	Sequence 23, Appl
45	9	45.0	13	1	US-09-798-260-81	Sequence 81, Appl
46	9	45.0	13	1	US-09-245-105A-45	Sequence 45, Appl
47	9	45.0	13	1	US-09-245-105A-47	Sequence 47, Appl
48	9	45.0	13	1	US-09-245-105A-51	Sequence 51, Appl
49	9	45.0	13	1	US-09-245-105A-53	Sequence 53, Appl
50	9	45.0	13	1	US-09-245-105A-59	Sequence 59, Appl
51	9	45.0	13	1	US-09-245-105A-61	Sequence 61, Appl
52	8.8	44.0	12	1	US-09-751-561-18	Sequence 18, Appl
53	8.8	44.0	12	1	US-09-751-561-20	Sequence 20, Appl
54	8.8	44.0	12	1	US-09-989-364-22	Sequence 22, Appl
55	8.8	44.0	12	1	US-09-989-364-24	Sequence 24, Appl
56	8.8	44.0	13	1	US-09-740-332-4616	Sequence 4616, Ap
57	8.8	44.0	13	1	US-09-817-879-4616	Sequence 4616, Ap
58	8.4	42.0	10	1	US-10-293-222-11	Sequence 11, Appl
59	8.4	42.0	10	1	US-10-033-145-17	Sequence 17, Appl
60	8.4	42.0	10	1	US-10-033-145-1384	Sequence 1384, Ap
61	8.4	42.0	10	1	US-10-330-627-406	Sequence 406, App
62	8.4	42.0	11	1	US-10-005-212-8	Sequence 8, Appl
63	8.4	42.0	11	1	US-10-441-495-21	Sequence 21, Appl
64	8.4	42.0	11	1	US-10-441-495-25	Sequence 25, Appl
65	8	40.0	10	1	US-09-777-207-15	Sequence 15, Appl
66	8	40.0	10	1	US-10-033-145-1287	Sequence 1287, Ap
67	8	40.0	10	1	US-10-033-145-1924	Sequence 1924, Ap
68	8	40.0	10	1	US-10-079-954-3	Sequence 3, Appl
69	8	40.0	10	1	US-10-033-717-22	Sequence 22, Appl
70	8	40.0	10	1	US-10-330-627-83	Sequence 83, Appl
71	8	40.0	11	1	US-09-796-071-39	Sequence 39, Appl
72	8	40.0	11	1	US-10-314-322-312	Sequence 312, App
73	7.8	39.0	11	1	US-09-263-959-809	Sequence 809, App
74	7.8	39.0	11	1	US-09-263-959-955	Sequence 955, App
75	7.8	39.0	11	1	US-09-816-277-62	Sequence 62, Appl
76	7.8	39.0	11	1	US-10-053-526A-4	Sequence 4, Appl
77	7.8	39.0	11	1	US-10-224-836-196	Sequence 196, App
78	7.8	39.0	11	1	US-10-080-979-14	Sequence 14, Appl
79	7.8	39.0	12	1	US-09-777-430A-57	Sequence 57, Appl
80	7.8	39.0	12	1	US-10-001-670-78	Sequence 78, Appl
81	7.8	39.0	12	1	US-10-001-670-79	Sequence 79, Appl
82	7.8	39.0	12	1	US-10-084-839-3010	Sequence 3010, Ap
83	7.8	39.0	12	1	US-10-312-273-653	Sequence 653, App
84	7.4	37.0	9	1	US-09-989-789-2216	Sequence 2216, Ap
85	7.4	37.0	9	1	US-09-989-789-2286	Sequence 2286, Ap
86	7.4	37.0	9	1	US-09-989-789-2287	Sequence 2287, Ap
87	7.4	37.0	9	1	US-09-990-186-2216	Sequence 2216, Ap
88	7.4	37.0	9	1	US-09-990-186-2286	Sequence 2286, Ap
89	7.4	37.0	9	1	US-09-990-196-2287	Sequence 2287, Ap
90	7.4	37.0	9	1	US-09-989-994-2216	Sequence 2216, Ap
91	7.4	37.0	9	1	US-09-989-994-2286	Sequence 2286, Ap
92	7.4	37.0	9	1	US-09-989-994-2287	Sequence 2287, Ap
93	7.4	37.0	9	1	US-10-096-596-15	Sequence 15, Appl
94	7.4	37.0	9	1	US-10-076-047A-65	Sequence 65, Appl
95	7.4	37.0	9	1	US-10-076-047A-67	Sequence 67, Appl
96	7.4	37.0	10	1	US-09-772-105-80	Sequence 80, Appl
97	7.4	37.0	10	1	US-09-989-789-567	Sequence 567, App
98	7.4	37.0	10	1	US-09-989-789-568	Sequence 568, App
99	7.4	37.0	10	1	US-09-772-719-21	Sequence 21, Appl
100	7.4	37.0	10	1	US-09-990-186-567	Sequence 567, App
101	7.4	37.0	10	1	US-09-990-186-568	Sequence 568, App
102	7.4	37.0	10	1	US-09-915-443A-1	Sequence 1, Appl
103	7.4	37.0	10	1	US-09-989-994-567	Sequence 567, App
104	7.4	37.0	10	1	US-09-989-994-568	Sequence 568, App
105	7.4	37.0	10	1	US-10-257-021-109	Sequence 109, App
106	7.4	37.0	10	1	US-10-033-145-133	Sequence 133, App

c 107 7.4 37.0 10 1 US-10-033-145-475 Sequence 475, App
108 7.4 37.0 10 1 US-10-033-145-479 Sequence 479, App
109 7.4 37.0 10 1 US-10-033-145-546 Sequence 546, App
c 110 7.4 37.0 10 1 US-10-033-145-567 Sequence 567, App
111 7.4 37.0 10 1 US-10-033-145-1224 Sequence 1224, App
112 7.4 37.0 10 1 US-10-330-627-357 Sequence 357, App
113 7.4 37.0 10 1 US-10-330-627-656 Sequence 656, App
114 7.4 37.0 10 1 US-10-330-627-693 Sequence 693, App
115 7.4 37.0 10 1 US-10-330-627-1122 Sequence 1122, App
116 7.4 37.0 10 1 US-10-330-627-1226 Sequence 1226, App
117 7.4 37.0 10 1 US-10-330-627-1227 Sequence 1227, App
118 7.4 37.0 10 1 US-10-330-627-1368 Sequence 1368, App
c 119 7.4 37.0 10 1 US-10-197-019-97 Sequence 97, Appl
120 7.4 37.0 10 1 US-10-193-507-83 Sequence 83, Appl
c 121 7.4 37.0 10 1 US-10-642-322-80 Sequence 20, Appl
122 7.4 37.0 10 1 US-10-642-322-22 Sequence 22, Appl
123 7.4 37.0 10 1 US-09-249-155-89 Sequence 89, Appl
124 7.4 37.0 11 1 US-09-249-155-177 Sequence 177, Appl
c 125 7.4 37.0 11 1 US-09-918-715-9 Sequence 9, Appl
126 7.4 37.0 11 1 US-10-027-632-175703 Sequence 175703, Appl
c 127 7.4 37.0 11 1 US-10-027-632-175703 Sequence 175703, Appl
128 7.4 37.0 11 1 US-10-027-632-175712 Sequence 175712, Appl
c 129 7.4 37.0 11 1 US-10-027-632-175712 Sequence 175712, Appl
130 7.4 37.0 11 1 US-10-314-322-89 Sequence 89, Appl
131 7.4 37.0 11 1 US-10-314-322-89 Sequence 89, Appl
c 132 7.4 37.0 11 1 US-10-314-322-177 Sequence 177, App

ALIGNMENTS

RESULT 1
US-10-003-919-21
; Sequence 21, Application US/10003919
; Publication No. US20030114401A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
; FILE REFERENCE: RTS-0256
; CURRENT APPLICATION NUMBER: US/10/003,919
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-21

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTCGCTGGCAGCAGC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGACTCGCTGGCAGCAGC 20

RESULT 2
US-10-712-672-48
; Sequence 48, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-48
Query Match 61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 9;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGGACTCGCTGGCAGC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 UGCGCUCUCUGGCAGC 17

RESULT 3
US-09-790-264-28/C
; Sequence 28, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-790-264-28

Query Match 59.0%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 11;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAGC 16
| | | | | | | | | | | | | | | | | | | | | |
Db 17 TGGCTTCGAGGCAC 3

RESULT 4
US-10-269-353-28/c
; Sequence 28, Application US/10269353

Publication No. US20030104447A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI2000-5380MNCINIM
; CURRENT APPLICATION NUMBER: US/10/269,353
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-10-269-353-28

Query Match 59.0%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 11;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGACTCGCTGGCAC 16
DB 17 TGGCTCGCAGGCAC 3
RESULT 5
US-10-138-674-7618/c
; Sequence 7618, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7618

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGC 14
DB 17 TGTACTCGCTGGC 5
RESULT 6
US-10-138-674-7619/c
; Sequence 7619, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7619
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7619

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGC 14
DB 13 TGTACTCGCTGGC 1
RESULT 7
US-10-287-949A-7618/c
; Sequence 7618, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7618

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGC 14
DB 17 TGTACTCGCTGGC 5
RESULT 8
US-10-287-949A-7619/c
; Sequence 7619, Application US/10287949A
; Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 7619
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-7619

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGACTCGCTGGC 14
Db 13 TGTACTCGCTGGC 1

RESULT 9
US-10-712-672-619
Sequence 619, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowiriza, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBH00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 619
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-619

Query Match 57.0%; Score 11.4; DB 1; Length 17;
Best Local Similarity 76.9%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGCAGC 18
Db 4 CUCUCUGGCAGC 16

RESULT 10
US-09-866-108-9914/c
Sequence 9914, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6

APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeonica Sequence Listing Engine
SEQ ID NO 9914
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-9914

Query Match 56.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGACTCGCTGGC 16
Db 17 AGGACTCGCAGGAC 2

RESULT 11
US-09-866-108-9915/c
Sequence 9915, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6

Matches	10;	Conservative	3;	Mismatches	3;	Indels	0;	Gaps	0;
QY	2	TCGACTCGCTGGCAGC	17						
Db	2	UGCGCUCUCUGGCAGC	17						
<p>RESULT 13</p> <p>US-10-712-672-1569</p> <p>; Sequence 1569, Application US/10712672</p> <p>; Publication No. US20040102413A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Ribozyme Pharmaceuticals, Inc.</p> <p>; APPLICANT: Chowrira, Bharat</p> <p>; APPLICANT: McSwiggen, Jim</p> <p>; APPLICANT: Stinchcomb, Dan</p> <p>; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme</p> <p>; FILE REFERENCE: MBH800-882-C (400/019)</p> <p>; CURRENT FILING DATE: 2003-11-13</p> <p>; PRIOR FILING DATE: 2003-11-13</p> <p>; PRIOR APPLICATION NUMBER: US/09/653,225</p> <p>; PRIOR FILING DATE: 2000-08-31</p> <p>; PRIOR APPLICATION NUMBER: 60/197,769</p> <p>; PRIOR FILING DATE: 2000-04-14</p> <p>; PRIOR APPLICATION NUMBER: 60/150,713</p> <p>; PRIOR FILING DATE: 1999-08-31</p> <p>; NUMBER OF SEQ ID NOS: 5586</p> <p>; SOFTWARE: PatentIn version 3.0</p> <p>; SEQ ID NO 1569</p> <p>; LENGTH: 16</p> <p>; TYPE: RNA</p> <p>; ORGANISM: Homo sapiens</p> <p>US-10-712-672-1569</p>									
<p>Query Match 54.0%; Score 10.8; DB 1; Length 16;</p> <p>Best Local Similarity 71.4%; Pred. No. 17;</p> <p>Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;</p>									
QY	7	TCGCTGGCAGGCAC	20						
Db	1	UCUCUGGCAGGCAC	14						
<p>RESULT 14</p> <p>US-10-312-273-661/c</p> <p>; Sequence 661, Application US/10312273</p> <p>; Publication No. US20040005667A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: CHIRON SDA</p> <p>; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE</p> <p>; FILE REFERENCE: P025035WO</p> <p>; CURRENT APPLICATION NUMBER: US/10/312,273</p> <p>; CURRENT FILING DATE: 2002-12-20</p> <p>; PRIOR APPLICATION NUMBER: 0016363.4</p> <p>; PRIOR FILING DATE: 2000-07-03</p> <p>; PRIOR APPLICATION NUMBER: 0017047.2</p> <p>; PRIOR FILING DATE: 2000-07-11</p> <p>; PRIOR APPLICATION NUMBER: 0017983.8</p> <p>; PRIOR FILING DATE: 2000-07-21</p> <p>; PRIOR APPLICATION NUMBER: 0019368.0</p> <p>; PRIOR FILING DATE: 2000-08-07</p> <p>; PRIOR APPLICATION NUMBER: 0020440.4</p> <p>; PRIOR FILING DATE: 2000-08-18</p> <p>; PRIOR APPLICATION NUMBER: 0022583.9</p> <p>; PRIOR FILING DATE: 2000-09-14</p> <p>; PRIOR APPLICATION NUMBER: 0027549.5</p> <p>; PRIOR FILING DATE: 2000-11-10</p> <p>; PRIOR APPLICATION NUMBER: 0031706.5</p> <p>; PRIOR FILING DATE: 2000-12-22</p> <p>; NUMBER OF SEQ ID NOS: 664</p> <p>; SOFTWARE: SeqWin99, version 1.02</p> <p>; SEQ ID NO 661</p> <p>; LENGTH: 12</p>									

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer tail
US-10-312-273-661

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCTGCGACGCAC 20
||| |||||
DB 12 GCTAGCAGGCAC 1

RESULT 15

US-09-848-754A-9285/c
; Sequence 9285, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9285
; LENGTH: 15

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-9285

Query Match 52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGC 17
|||||
DB 12 CTCGCTGGCAGC 1

RESULT 16

US-10-160-388-9/c
; Sequence 9, Application US/10160388
; Publication No. US20040072161A1
; GENERAL INFORMATION:

; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Monroe, Glen
; APPLICANT: Sanchis, Angela
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE F2RL1 GENE
; FILE REFERENCE: F2RL1.MWH-1785US
; CURRENT APPLICATION NUMBER: US/10/160,388
; CURRENT FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: PCT/US01/46475
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/247,516
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-160-388-9

Query Match 52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.8%; Pred. No. 19;

Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGACTCGCTGGCAGC 16
||| |||||
DB 14 GGTCTCCTGTGCAC 1

RESULT 17

US-10-435-696-232/c
; Sequence 232, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:

; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 16

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D17S946 reverse primer

US-10-435-696-232

Query Match 52.0%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGC 17
|||||
DB 15 CTCCTGGCAGC 4

RESULT 18

US-10-138-674-5820/c
; Sequence 5820, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5820
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-138-674-5820

Query Match 52.0%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
|||||
DB 16 GTACTCGCTGGC 5

```
RESULT 19
US-10-287-949A-5820/c
; Sequence 5820, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEH800-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5820
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5820

Query Match          52.0%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
DB 16 GACTCGCTGGC 5

RESULT 20
US-09-825-805-143
; Sequence 143, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MEH800-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-143

Query Match          51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
Best Local Similarity 66.7%; Pred. No. 21;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGC 16
DB 1 UGGAGCGCGUGACAC 15

RESULT 21
US-09-740-332-4783
; Sequence 4783, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: REI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4783
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4783

Query Match          51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACTCGCTGGCAGC 18
DB 1 GACUCGUAGGCUCGC 15

RESULT 22
US-09-817-879-4783
; Sequence 4783, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MEH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4783
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4783

Query Match          51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACTCGCTGGCAGC 18
DB 1 GACUCGUAGGCUCGC 15

RESULT 23
```

```
US-10-339-674-740
; Sequence 740, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 740
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (744543)...(744657)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 965
US-10-339-674-740

Query Match      51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGACTCGCTGGCA 15
Db 1 ATGGCGCGCTGGCA 15

RESULT 24
US-10-339-674-1891
; Sequence 1891, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1891
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2576140)...(2576154)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2506
US-10-339-674-1891

Query Match      51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGACTCGCTGGCA 15
Db 1 ATGGCGCGCTGGCA 15

RESULT 25
US-10-096-718-9
; Sequence 9, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
```

```
US-10-096-718-29/c
; Sequence 29, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-29

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCAC 20
Db 2 TGGCAGCGCAC 11

RESULT 26
US-10-096-718-29/c
; Sequence 29, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-29

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCAC 20
Db 11 TGGCAGCGCAC 2

RESULT 27
US-10-347-510A-105
; Sequence 105, Application US/10347510A
; Publication No. US20040063110A1
; GENERAL INFORMATION:
; APPLICANT: Henrik Stender
; Kaare Lund
; Tina Anderson Hollerup
; TITLE OF INVENTION: No. US20040063110A1e1 Process For The Detection of Mycobacte
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
; STREET: 1300 I ST. NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: ASCxi
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/347,510A
; FILING DATE: 21-Jan-2003
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,392
; FILING DATE: 15-Oct-96
; APPLICATION NUMBER: 60/029,595
; FILING DATE: 23-Oct-96
; APPLICATION NUMBER: 60/045,962
; FILING DATE: 08-May-97
; APPLICATION NUMBER: 08/943,777
; FILING DATE: 3-Oct-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Anthony C. Tridico
; REGISTRATION NUMBER: 45,958
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4173
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 basepairs
; TYPE: nucleic acid basepairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-347-510A-105

Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 17
DB 5 CGCTGGCAGC 14

RESULT 28
US-09-544-934B-105
; Sequence 105, Application US/09544934B
; Publication No. US20020137035A1
; GENERAL INFORMATION:
; APPLICANT: Henrik Stender
; Kaare Lund
; TITLE OF INVENTION: Novel Process For The Detection of Mycobacteria
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, PARABOW, GARRETT, & DUNNER
; STREET: 1300 I ST. NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: ASCXI
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/544,934B
; FILING DATE: 07-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,392
; FILING DATE: 15-Oct-96
; APPLICATION NUMBER: 60/029,595
; FILING DATE: 23-Oct-96
; APPLICATION NUMBER: 60/045,962
; FILING DATE: 08-May-97
; APPLICATION NUMBER: 08/943,777
; FILING DATE: 3-Oct-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Anthony C. Tridico
; REGISTRATION NUMBER: 45,958
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4173
; TELEFAX: (202) 408-4400

```

```

; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 basepairs
; TYPE: nucleic acid basepairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-544-934B-105

Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 17
DB 5 CGCTGGCAGC 14

RESULT 29
US-10-189-956-30
; Sequence 30, Application US/10189956
; Publication No. US20030152951A1
; GENERAL INFORMATION:
; APPLICANT: Mirel, Daniel B
; APPLICANT: Erlich, Henry A
; APPLICANT: Bugawan, Teodorica L
; APPLICANT: No. US20030152951A1, Janelle A
; APPLICANT: Valdes, Ana M
; TITLE OF INVENTION: IL-4 RECEPTOR SEQUENCE VARIATION ASSOCIATED WITH TYPE 1
; TITLE OF INVENTION: DIABETES
; FILE REFERENCE: 1803-295-999
; CURRENT APPLICATION NUMBER: US/10/189,956
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-189-956-30

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGCA 15
DB 3 GGCTCCCTGGCA 15

RESULT 30
US-10-138-674-4143
; Sequence 4143, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens

```

US-10-138-674-4143									
Query Match 49.0%; Score 9.8; DB 1; Length 15;									
Best Local Similarity 61.5%; Pred. No. 26;									
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGGACTCGCTGG	13						
DB	1	AUGGAUCUCUGG	13						
RESULT 31									
US-10-287-949A-4143									
; Sequence 4143, Application US/10287949A									
; Publication No. US20040102389A1									
; GENERAL INFORMATION: Directed Antisense Libraries									
; APPLICANT: Pavco, Pam									
; APPLICANT: McSwiggan, Jim									
; APPLICANT: Stinchcomb, Dan									
; APPLICANT: Escobedo, Jaime									
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re									
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor									
; FILE REFERENCE: MBH300-876-N (400/049)									
; CURRENT APPLICATION NUMBER: US/10/287,949A									
; CURRENT FILING DATE: 2003-04-11									
; NUMBER OF SEQ ID NOS: 20822									
; SOFTWARE: PatentIn version 3.0									
; SEQ ID NO 4143									
; LENGTH: 15									
; TYPE: RNA									
; ORGANISM: Homo sapiens									
US-10-287-949A-4143									
Query Match 49.0%; Score 9.8; DB 1; Length 15;									
Best Local Similarity 61.5%; Pred. No. 26;									
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGGACTCGCTGG	13						
DB	1	AUGGAUCUCUGG	13						
RESULT 32									
US-10-291-230-34									
; Sequence 34, Application US/10291230									
; Publication No. US20030108939A1									
; GENERAL INFORMATION: Directed Antisense Libraries									
; APPLICANT: Ruffner, Duane E.									
; APPLICANT: Chen, Zhidong									
; TITLE OF INVENTION: Directed Antisense Libraries									
; FILE REFERENCE: T6678.US.A									
; CURRENT APPLICATION NUMBER: US/10/291,230									
; CURRENT FILING DATE: 2002-11-07									
; PRIOR APPLICATION NUMBER: US 09/647,344									
; PRIOR FILING DATE: 2000-12-04									
; PRIOR APPLICATION NUMBER: PCT/US99/06742									
; PRIOR FILING DATE: 1999-03-28									
; PRIOR APPLICATION NUMBER: US 60/079,792									
; PRIOR FILING DATE: 1998-03-28									
; PRIOR APPLICATION NUMBER: US 60/107,504									
; PRIOR FILING DATE: 1998-11-06									
; NUMBER OF SEQ ID NOS: 50									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 34									
; LENGTH: 14									
; TYPE: DNA									
; ORGANISM: herpes simplex virus									
US-10-291-230-34									
Query Match 47.0%; Score 9.4; DB 1; Length 14;									
Best Local Similarity 90.9%; Pred. No. 30;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	3	GGACTCGCTGG	13						
DB	3	GGATTCGCTGG	13						
RESULT 33									
US-10-291-249-34									
; Sequence 34, Application US/10291249									
; Publication No. US20030119041A1									
; GENERAL INFORMATION: Directed Antisense Libraries									
; APPLICANT: Ruffner, Duane E.									
; APPLICANT: Pierce, Michael L.									
; APPLICANT: Chen, Zhidong									
; TITLE OF INVENTION: Directed Antisense Libraries									
; FILE REFERENCE: T6678.US.B									
; CURRENT APPLICATION NUMBER: US/10/291,249									
; CURRENT FILING DATE: 2002-11-07									
; PRIOR APPLICATION NUMBER: US 09/647,344									
; PRIOR FILING DATE: 2000-12-04									
; PRIOR APPLICATION NUMBER: PCT/US99/06742									
; PRIOR FILING DATE: 1999-03-28									
; PRIOR APPLICATION NUMBER: US 60/079,792									
; PRIOR FILING DATE: 1998-03-28									
; PRIOR APPLICATION NUMBER: US 60/107,504									
; PRIOR FILING DATE: 1998-11-06									
; NUMBER OF SEQ ID NOS: 50									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 34									
; LENGTH: 14									
; TYPE: DNA									
; ORGANISM: herpes simplex virus									
US-10-291-249-34									
Query Match 47.0%; Score 9.4; DB 1; Length 14;									
Best Local Similarity 90.9%; Pred. No. 30;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	3	GGACTCGCTGG	13						
DB	3	GGATTCGCTGG	13						
RESULT 34									
US-10-084-839-3847									
; Sequence 3847, Application US/10084839									
; Publication No. US20030186238A1									
; GENERAL INFORMATION: Directed Antisense Libraries									
; APPLICANT: Third Wave Technologies									
; APPLICANT: Allawi, Hatim									
; APPLICANT: Argue, Brad T.									
; APPLICANT: Bartholomay, Christian T.									
; APPLICANT: Chehak, LuAnne									
; APPLICANT: Curtis, Michelle L.									
; APPLICANT: Eis, Peggy S.									
; APPLICANT: Hall, Jeff G.									
; APPLICANT: Ip, Hon S.									
; APPLICANT: Ji, Lin									
; APPLICANT: Kaiser, Michael									
; APPLICANT: Kwiatkowski, Jr., Robert W.									
; APPLICANT: Lukowiak, Andrew A.									
; APPLICANT: Lyamichev, Victor									
; APPLICANT: Lymaicheva, Natalie E.									
; APPLICANT: Ma, Wupo									
; APPLICANT: Neri, Bruce P.									
; APPLICANT: Olson, Sarah M.									
; APPLICANT: Olson-Munoz, Marilyn C.									
; APPLICANT: Schaefer, James J.									
; APPLICANT: Skrzypczynski, Zbigniew									
; APPLICANT: Takova, Tsetska Y.									
; APPLICANT: Thompson, Lisa C.									
; APPLICANT: Vedvik, Kevin L.									
US-10-084-839-3847									
Query Match 47.0%; Score 9.4; DB 1; Length 14;									
Best Local Similarity 90.9%; Pred. No. 30;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	3	GGACTCGCTGG	13						
DB	3	GGATTCGCTGG	13						

```
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3847
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3847

Query Match          47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGGCAGCAC 20
    |||||
Db 1 CTGGCACTCAC 11

RESULT 35
US-10-033-145-833
; Sequence 833, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 833
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-833

Query Match          45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
    |||||
Db 2 TGGCAGCGCA 10

RESULT 36
US-10-033-145-1372/c
; Sequence 1372, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1372
; LENGTH: 10
; TYPE: DNA
US-10-033-145-1372

; ORGANISM: Homo sapiens
US-10-033-145-1372

Query Match          45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGCACGCGAC 20
    |||||
Db 9 GGCACGCGAC 1

RESULT 37
US-10-330-627-1189
; Sequence 1189, Application US/10330627
; Publication No. US2003017577A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1189
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1189

Query Match          45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
    |||||
Db 2 TGGCAGCGCA 10

RESULT 38
US-09-238-351-45/c
; Sequence 45, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kaytem, Jon Faiz
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; CURRENT FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
```

```
US-09-238-351-45
Query Match          45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 10 ATGGACTCG 2

RESULT 39
US-09-238-351-47/c
; Sequence 47, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-47

Query Match          45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 10 ATGGACTCG 2

RESULT 40
US-09-238-351-51/c
; Sequence 51, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-51

Query Match          45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 10 ATGGACTCG 2

RESULT 41
US-09-238-351-53/c
; Sequence 53, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-53

Query Match          45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 10 ATGGACTCG 2

RESULT 42
US-09-238-351-59/c
; Sequence 59, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; EARLIER FILING DATE: 1999-01-27
```


; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-59

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
| | | | | | | | | | | | | | |
Db 10 ATGGACTCG 2

RESULT 43
US-09-238-351-61/c
; Sequence 61, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayvem, Jon Faiz
; APPLICANT: Bandad, Cynthia
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; TITLE OF INVENTION: Detection
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; CURRENT FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-61

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
| | | | | | | | | | | | | | |
Db 10 ATGGACTCG 2

RESULT 44
US-09-510-378-23/c
; Sequence 23, Application US/09510378

; Publication No. US20030165823A1
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; Miyada, Charles Garrett
; Hubbell, Earl A.
; Chee, Mark
; Fodor, Stephen P.A.
; Huang, Xiaohua C.
; Lipshutz, Robert J.
; Lobban, Peter E.
; Morris, Macdonald S.
; Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/510,378
; FILING DATE: 22-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/544,381
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-510-378-23

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
| | | | | | | | | | | | | | |
Db 11 GGCACGCAC 3

RESULT 45
US-09-798-260-81/c
; Sequence 81, Application US/09798260
; Publication No. US20030165830A1
; GENERAL INFORMATION:

```

Query Match          45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY      12 GGCAGGCAC 20
      |||||
DB       11 GGCAGGCAC 3

RESULT 46
US-09-245-105A-45/c
; Sequence 45, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Banded, Cynthia
; APPLICANT: Yu, Changjun
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Mo
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-45

```

```

Query Match          45.0%; Score 9; DB 1; Length 13;
Best local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  ATGGACTCG 9
          |||||
Db      10 ATGGACTCG 2

RESULT 48
US-09-245-105A-51/c
; Sequence 51, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Yu, Changjun
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-51

```

Query Match 45.0%; Score 9; DB 1; Length 13;

rnp

Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 49
US-09-245-105A-53/c
; Sequence 53, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-53

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 50
US-09-245-105A-59/c
; Sequence 59, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-59

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 51
US-09-245-105A-61/c
; Sequence 61, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Yu, Changjun
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-61

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 52
US-09-751-561-18
; Sequence 18, Application US/09751561
; Patent No. US20010007985A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214

```
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7934-015-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)-790-9090
/ TELEFAX: (212)-869-8864
/ TELEX: 66441 PENNIE
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-09-751-561-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 53
US-09-751-561-20
; Sequence 20, Application US/09751561
; Patent No. US20010007985A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7934-015-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)-790-9090
/ TELEFAX: (212)-869-8864
/ TELEX: 66441 PENNIE
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
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```
US-09-751-561-20

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGGCG 12

RESULT 54
US-09-989-364-22
; Sequence 22, Application US/09989364
; Publication No. US20030003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Kinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-22

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 55
US-09-989-364-24
; Sequence 24, Application US/09989364
; Publication No. US20030003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Kinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-24

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 5 ACTCGCTGGCAC 16
 Db 1 AGTCGCTGGCGC 12

RESULT 56
 US-09-740-332-4616/c
 ; Sequence 4616, Application US/09740332
 ; Publication No. US20030125270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
 ; FILE REFERENCE: RPI 400/003
 ; CURRENT APPLICATION NUMBER: US/09/740,332
 ; CURRENT FILING DATE: 2001-03-26
 ; NUMBER OF SEQ ID NOS: 9704
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4616
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION:
 ; OTHER INFORMATION: oligonucleotide substrate
 US-09-740-332-4616

Query Match 44.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
 Db 12 ACTCGCAAGCAC 1

RESULT 57
 US-09-817-879-4616/c
 ; Sequence 4616, Application US/09817879
 ; Publication No. US2003017131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
 ; FILE REFERENCE: MEH800-801-F
 ; CURRENT APPLICATION NUMBER: US/09/817,879
 ; CURRENT FILING DATE: 2001-03-26
 ; NUMBER OF SEQ ID NOS: 9703
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4616
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION:
 ; OTHER INFORMATION: oligonucleotide substrate
 US-09-817-879-4616

Query Match 44.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
 Db 12 ACTCGCAAGCAC 1

RESULT 58
 US-10-293-222-11/c
 ; Sequence 11, Application US/10293222

; Publication No. US20040033932A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Versteeg, Rogier
 ; TITLE OF INVENTION: MYC targets
 ; FILE REFERENCE: 2183-5580US
 ; CURRENT APPLICATION NUMBER: US/10/293,222
 ; CURRENT FILING DATE: 2002-11-12
 ; PRIOR APPLICATION NUMBER: PCT/NL01/00361
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: EP 00201698.8
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: EP 00202284.6
 ; PRIOR FILING DATE: 2000-06-29
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-293-222-11

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 38;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGCAC 20
 Db 10 TGGCAGCGAAC 1

RESULT 59
 US-10-033-145-17
 ; Sequence 17, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-17

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 38;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCTGG 13
 Db 1 GACCCGCTGG 10

RESULT 60
 US-10-033-145-1384
 ; Sequence 1384, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145

```
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1384
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1384

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCTGGCAGGC 18
DB 1 GCTGGCAGGC 10

RESULT 61
US-10-330-627-406/c
; Sequence 406, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-406

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
DB 10 TGGCAGGAAC 1

RESULT 62
US-10-005-212-8
; Sequence 8, Application US/10005212
; Publication No. US20020193570A1
; GENERAL INFORMATION:
; APPLICANT: GILLIES, Stephen D
; APPLICANT: LAN, Yan
; APPLICANT: LO, Kin-Ming
; TITLE OF INVENTION: Heterodimeric Fusion Proteins Useful for Targeted
; FILE REFERENCE: LEX-002C1
; CURRENT APPLICATION NUMBER: US/10/005,212
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: USSN 08/986,997
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-10-005-212-8

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCGC 10
DB 2 ATGGACTTGC 11

RESULT 63
US-10-441-495-21
; Sequence 21, Application US/10441495
; Publication No. US20040005613A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040005613A1ton, Michael
; TITLE OF INVENTION: Methods, Probes, and Accessory Molecules for Detecting Single
; FILE REFERENCE: MU-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/441,495
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/383,291
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/387,831
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-441-495-21

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCGA 19
DB 2 CTGGCAGGTA 11

RESULT 64
US-10-441-495-25/c
; Sequence 25, Application US/10441495
; Publication No. US20040005613A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040005613A1ton, Michael
; TITLE OF INVENTION: Methods, Probes, and Accessory Molecules for Detecting Single
; FILE REFERENCE: MU-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/441,495
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/383,291
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/387,831
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-441-495-25

Query Match      42.0%; Score 8.4; DB 1; Length 11;
```

Best Local Similarity 90.0%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCA 19
| | | | |
Db 10 CTGGCAGCA 1

RESULT 65

US-10-033-145-1287/c
; Sequence 15, Application US/09777207
; Publication No. US20020039780A1
; GENERAL INFORMATION:
; APPLICANT: HORVATH, DIANA M.
; APPLICANT: CHUA, NAM-HAI
; APPLICANT: STUIVER, MAARTEN H.
; APPLICANT: JEPSON, IAN
; TITLE OF INVENTION: New Salicylic Acid Inducible Genes and Promoters
; CURRENT APPLICATION NUMBER: US/09/777,207
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US60/095,187
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence Primer API
US-09-777-207-15

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
| | | | |
Db 9 TCGCTGGC 2

RESULT 66

US-10-033-145-1287/c
; Sequence 1287, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1287

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTCG 9
| | | | |
Db 10 TGGACTCG 3

RESULT 67

US-10-033-145-1924
; Sequence 1924, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1924
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1924

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGGC 18
| | | | |
Db 2 TGGCAGGC 9

RESULT 68

US-10-079-954-3/c
; Sequence 3, Application US/10079954
; Publication No. US20020168661A1
; GENERAL INFORMATION:
; APPLICANT: DURST, MATTHIAS
; APPLICANT: NEES, MATTHIAS
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/10/079,954
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US/09/308,984
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DS97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-954-3

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
| | | | |
Db 9 TCGCTGGC 2

RESULT 69

US-10-033-717-22/c
; Sequence 22, Application US/10033717
; Publication No. US20030078406A1
; GENERAL INFORMATION:
; APPLICANT: BLAIR, DONALD
; APPLICANT: CLAUSEN, PETER
; APPLICANT: TOPOL, LILIA
; APPLICANT: MARX, MARIA

APPLICANT: CALOTHY, GEORGES
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DEM, A SECRETED PROTEIN
FILE REFERENCE: 14014.0358
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: US/10/033,717
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/444,066
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/079,440
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence./No. US20030078406A1e =
US-10-033-717-22

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
DB 9 TCGCTGGC 2

RESULT 70
US-10-330-627-83
Sequence 83, Application US/10330627
Publication No. US2003017571A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-627-83

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
DB 3 ATGGACTC 10

RESULT 71
US-09-796-071-39
Sequence 39, Application US/09796071
Patent No. US2002012925A1
GENERAL INFORMATION:
APPLICANT: Chee, Mark S.
TITLE OF INVENTION: Computer-Aided Visualization and Analysis System for Sequence Evaluation
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ritter, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: California
COUNTRY: USA
ZIP: 94022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatenIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/796,071
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/531,137
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ritter, Michael J.
REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: APFP006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-903-3500
TELEFAX: 650-903-3501
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-796-071-39

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGGCAGC 17
DB 1 CTGGCAGC 8

RESULT 72
US-10-314-322-312/c
Sequence 312, Application US/10314322
Publication No. US2003022991A1
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound Healing
FILE REFERENCE: 000486.00016
CURRENT APPLICATION NUMBER: US/10/314,322
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/074,737
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/097,937
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/102,051
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: US 09/249,155
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 346
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 11
TYPE: DNA
ORGANISM: Mus musculus
US-10-314-322-312

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCA 19
|||||
Db 11 GGCACGCA 4

RESULT 73

US-09-263-959-809
; Sequence 809, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Rowen, Lee
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 809:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

US-09-263-959-809
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
|||||
Db 1 GCAGGCAGCA 11

```
; APPLICANT: INSTITUT CURIE; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.);
; APPLICANT: MUSEUM NATIONAL D'HISTOIRE NATURELLE; INSTITUT NATIONAL DE LA SANTE ET DE
; APPLICANT: RECHERCHE MEDICALE (INSERM)
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Blodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 3754/0K213
; CURRENT APPLICATION NUMBER: US/10/053,526A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526A-4

Query Match          39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 18
Db 11 CGCTGGCAGC 1

RESULT 77
US-10-224-836-196
; Sequence 196, Application US/10224836
; Publication No. US20030082598A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Molecular Interaction Sites Of 23S Ribosomal RNA And Methods Of
; TITLE OF INVENTION: Modulating The Same
; FILE REFERENCE: IBIS0402
; CURRENT APPLICATION NUMBER: US/10/224,836
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/314,251
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 11
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-224-836-196

Query Match          39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGGCAGC 17
Db 1 UCGCUGAGAGC 11

RESULT 78
US-10-080-979-14/c
; Sequence 14, Application US/10080979
; Publication No. US20030191075A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan
```

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; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bennett, Frank C.
; TITLE OF INVENTION: Oligonucleotide Conjugates For Hepatic Delivery
; FILE REFERENCE: IS-5028
; CURRENT APPLICATION NUMBER: US/10/080,979
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (6)-(6)
; OTHER INFORMATION: hexyl-(N-phthalimido)amino]-uridine
US-10-080-979-14

Query Match          39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 18
Db 11 CGCAGACAGC 1

RESULT 79
US-09-777-430A-57
; Sequence 57, Application US/09777430A
; Patent No. US20020128465A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Allawi, Hatim T.
; APPLICANT: Wayland, Sarah R.
; APPLICANT: Takova, Tssetska
; APPLICANT: Neir, Bruce P.
; TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
; FILE REFERENCE: FORS-04912
; CURRENT APPLICATION NUMBER: US/09/777,430A
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-777-430A-57

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 18
Db 1 CGCTGTCTGC 11

RESULT 80
US-10-001-670-78
; Sequence 78, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rochberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
```

US-10-001-670-78
CURRENT APPLICATION NUMBER: US/10/001,670
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/231,303
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 08/663,824
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-78
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGACTCGCTG 12
Db 1 TCGAGTCGCTG 11
RESULT 81
US-10-001-670-79
Sequence 79, Application US/10001670
Publication No. US20030119002A1
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
INTERACTIONS THAT OCCUR IN POPULATIONS AND
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
FILE REFERENCE: 7934-087
CURRENT APPLICATION NUMBER: US/10/001,670
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/231,303
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 08/663,824
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 79
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-79
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGACTCGCTG 12
Db 1 TCGAGTCGCTG 11
RESULT 82
US-10-084-839-3010
Sequence 3010, Application US/10084839
Publication No. US2003018623A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allawi, Hatim
APPLICANT: Atque, Brad T.
APPLICANT: Bartholomay, Christian T.
APPLICANT: Chehak, LuAnne
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.

US-10-084-839-3010
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lymaicheva, Natalie E.
APPLICANT: Ma, WuPo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3010
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3010
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGACTCGCTGG 13
Db 2 GCACCCGCTGG 12
RESULT 83
US-10-312-273-663/c
Sequence 663, Application US/10312273
Publication No. US20040005667A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: P025035WO
CURRENT APPLICATION NUMBER: US/10/312,273
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 0017047.2
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 0017983.8
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 0019368.0
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 0020440.4
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 0022583.9
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 0027549.5
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 0031706.5
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 664
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 663
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Primer tail
US-10-312-273-663

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CTGGACGCAC 20
DB 11 CTAGTACGCAC 1

RESULT 84
US-09-989-789-2216
; Sequence 2216, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2216

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 85
US-09-989-789-2286
; Sequence 2286, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2286
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2286

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 86
US-09-989-789-2287
; Sequence 2287, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2287
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2287

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 87
US-09-990-186-2216
; Sequence 2216, Application US/09990186
; Publication No. US2003008675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2216

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 88
US-09-990-186-2286
; Sequence 2286, Application US/09990186
; Publication No. US2003008675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186

OTHER INFORMATION: Primer tail
US-10-312-273-663

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CTGGACGCAC 20
DB 11 CTAGTACGCAC 1

RESULT 84
US-09-989-789-2216
; Sequence 2216, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2216

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 85
US-09-989-789-2286
; Sequence 2286, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2286
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2286

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 86
US-09-989-789-2287
; Sequence 2287, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2287
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2287

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 87
US-09-990-186-2216
; Sequence 2216, Application US/09990186
; Publication No. US2003008675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2216

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9

RESULT 88
US-09-990-186-2286
; Sequence 2286, Application US/09990186
; Publication No. US2003008675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186

US-10-096-596-15/c
; Sequence 15, Application US/10096596
; Publication No. US20030049653A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for Breast Cancer
; FILE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-076-047A-67

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTGCTGG 13
|||||
Db 9 ACTGCTGG 1

RESULT 94
US-10-076-047A-65/c
; Sequence 65, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for Breast Cancer
; FILE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-076-047A-65

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
|||||
Db 9 CTGGCAGC 1

RESULT 95
US-10-076-047A-67/c
; Sequence 67, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for Breast Cancer
; FILE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-076-047A-67

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
|||||
Db 9 CTGGCAGC 1

RESULT 96
US-09-772-105-80/c
; Sequence 80, Application US/09772105
; Patent No. US20010029015A1
; GENERAL INFORMATION:
; APPLICANT: Ozelius, Laurie J.
; TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND
; FILE OF INVENTION: METHODS OF DETECTING NEURONAL DISEASES
; FILE REFERENCE: 0838.1001009
; CURRENT APPLICATION NUMBER: US/09/772,105
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/218,363
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/099,454
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/050,244
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exon/intron of TORB
; US-09-772-105-80

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCG 10
|||||
Db 9 TGGACTCAG 1

RESULT 97
US-09-989-789-567/c
; Sequence 567, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang

;; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
;; FILE REFERENCE: 8325-0011.20 / S11-US2
;; CURRENT APPLICATION NUMBER: US/09/989,789
;; CURRENT FILING DATE: 2002-03-25
;; NUMBER OF SEQ ID NOS: 4085
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 567
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example target
;; OTHER INFORMATION: DNA
US-09-989-789-567

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
||| ||| |||
DB 9 CGCTGGCAC 1

RESULT 98

US-09-989-789-568/c
;; Sequence 568, Application US/09989789
;; Patent No. US20020063379A1
;; GENERAL INFORMATION:
;; APPLICANT: LIU, Qiang
;; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
;; FILE REFERENCE: 8325-0011.20 / S11-US2
;; CURRENT APPLICATION NUMBER: US/09/989,789
;; CURRENT FILING DATE: 2002-03-25
;; NUMBER OF SEQ ID NOS: 4085
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 568
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example target
;; OTHER INFORMATION: DNA
US-09-989-789-568

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
||| ||| |||
DB 9 CGCTGGCAC 1

RESULT 99

US-09-772-719-21/c
;; Sequence 21, Application US/09772719
;; Patent No. US20020137910A1
;; GENERAL INFORMATION:
;; APPLICANT: Zavada, Jan
;; APPLICANT: Pastorekova, Silvia
;; APPLICANT: Pastorek, Jaromir
;; TITLE OF INVENTION: MN Gene and Protein
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Leona L. Lauder
;; STREET: 369 Pine Street
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94104

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/772,719
;; FILING DATE: 30-JAN-2001
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/485,049
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/260,190
;; FILING DATE: 15-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lauder, Leona L.
;; REGISTRATION NUMBER: 30,863
;; REFERENCE/DOCKET NUMBER: D-0021.3E
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-981-2034
;; TELEFAX: 415-981-0332
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; DESCRIPTION: P53 binding site
;; PUBLICATION INFORMATION:
;; AUTHORS: El Deiry et al.
;; TITLE: "Human genomic DNA sequences define a
;; TITLE: consensus binding site for p53"
;; JOURNAL: Nature Genetics
;; VOLUME: 1
;; PAGES: 44-49
;; DATE: 1992
;; US-09-772-719-21

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
||| ||| |||
DB 10 GGACTAGCT 2

RESULT 100

US-09-990-186-567/c
;; Sequence 567, Application US/09990186
;; Publication No. US20030068675A1
;; GENERAL INFORMATION:
;; APPLICANT: LIU, Qiang
;; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
;; FILE REFERENCE: 8325-0011.21 / S11-US3
;; CURRENT APPLICATION NUMBER: US/09/990,186
;; CURRENT FILING DATE: 2001-11-20
;; NUMBER OF SEQ ID NOS: 4085
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 567
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example target
;; OTHER INFORMATION: DNA
US-09-990-186-567

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      8 CGCTGGCAC 16
      |||||
Db      9 CGCTGCCAC 1

RESULT 101
US-09-990-186-568/c
; Sequence 568, Application US/09990186
; Publication No. US2003006875A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 568
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-568

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 CGCTGGCAC 16
      |||||
Db      9 CGCTGCCAC 1

RESULT 102
US-09-916-443A-1
; Sequence 1, Application US/09916443A
; Publication No. US2003009945A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Bruce
; APPLICANT: Tarasow, Theodore
; TITLE OF INVENTION: Parallel Selex
; FILE REFERENCE: 2636-108-C-II
; CURRENT APPLICATION NUMBER: US/09/916,443A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 09/546,657
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 09/157,601
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US 08/618,700
; PRIOR FILING DATE: 1996-03-20
; PRIOR APPLICATION NUMBER: US 08/309,245
; PRIOR FILING DATE: 1994-09-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Random Sequence
US-09-916-443A-1

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      10 CTGCGCAGC 18
      |||||
Db      2 CAGCGCAGC 10

RESULT 103
US-09-989-994-567/c
; Sequence 567, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-567

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 CGCTGGCAC 16
      |||||
Db      9 CGCTGCCAC 1

RESULT 104
US-09-989-994-568/c
; Sequence 568, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 568
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-568

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 CGCTGGCAC 16
      |||||
Db      9 CGCTGCCAC 1

RESULT 105
US-10-257-021-109/c
; Sequence 109, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.

```



```
Db      2 TGGCAGGCA 10

RESULT 110
US-10-033-145-567/c
; Sequence 567, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 567
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-567

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CTCGCTGGC 14
Db      10 CTCGCTGGC 2

RESULT 111
US-10-033-145-1224
; Sequence 1224, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1224
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1224

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCAGGCA 19
Db      2 TGGCAGCA 10

RESULT 112
US-10-033-627-357
; Sequence 357, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: HUMAN TRANSCRIPTOMES
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 10
; TYPE: DNA
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```
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-357

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 TCGCTGGCA 15
Db      1 TCGCTGGCA 9

RESULT 113
US-10-330-627-656
; Sequence 656, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 656
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-656

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CTCGCTGGC 14
Db      2 CTCGCTGGC 10

RESULT 114
US-10-330-627-693
; Sequence 693, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-330-627-693

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGGCAGCG 18
Db 2 CAGGCAGCG 10

RESULT 115
US-10-330-627-1122
; Sequence 1122, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1122
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1122

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 116
US-10-330-627-1226
; Sequence 1226, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1226
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1226

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 117
US-10-330-627-1227
; Sequence 1227, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1227
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1227

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 118
US-10-330-627-1368
; Sequence 1368, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1368
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1368

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GGCAGCGCAC 20
Db 1 GGCAGCGCAC 9

RESULT 119
US-10-197-019-97/c
; Sequence 97, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
```

; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-97

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14
Db 10 CCCGCTGGC 2

RESULT 120

US-10-197-019-98
; Sequence 98, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-98

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14
Db 2 CCCGCTGGC 10

RESULT 121

US-10-193-507-83/c
; Sequence 83, Application US/10193507
; Publication No. US20040018493A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Kazemi, Amir
; APPLICANT: Lachowicz, Michael F.
; APPLICANT: Pabon, Vicente
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFERENCE: MMH-2790US
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-507-83

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCGCTG 12
Db 10 GACTCCCTG 2

RESULT 122

US-10-642-322-20/c
; Sequence 20, Application US/10642322
; Publication No. US20040077080A1
; GENERAL INFORMATION:
; APPLICANT: Raucy, Judy
; TITLE OF INVENTION: Composition and Methods for Induction of Proteins Involved in
; TITLE OF INVENTION: Xenobiotic Metabolism
; FILE REFERENCE: PUR-00114.P.1.1.1.1
; CURRENT APPLICATION NUMBER: US/10/642,322
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/222,679
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 09/832,621
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/196,681
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/241,391
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-642-322-20

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCGCAGCA 19
Db 10 TCGCAGCA 2

RESULT 123

US-10-642-322-22
; Sequence 22, Application US/10642322
; Publication No. US20040077080A1
; GENERAL INFORMATION:
; APPLICANT: Raucy, Judy
; TITLE OF INVENTION: Composition and Methods for Induction of Proteins Involved in
; TITLE OF INVENTION: Xenobiotic Metabolism
; FILE REFERENCE: PUR-00114.P.1.1.1.1
; CURRENT APPLICATION NUMBER: US/10/642,322
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/222,679
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 09/832,621
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/196,681
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/241,391
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-642-322-22

Query Match          37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGCA 19
Db 1 TCGCAGCGCA 9

RESULT 124
US-09-249-155-89
; Sequence 89, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; PRIOR FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 89
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-89

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 1 ACTGGCTGG 9

RESULT 125
US-09-249-155-177/c
; Sequence 177, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; PRIOR FILING DATE: 1998-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 177
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-177

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 1 ACTGGCTGG 9

RESULT 126
US-09-918-715-9
; Sequence 9, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-9

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TCGCTGGCA 15
Db 1 TCCCTGGCA 9

RESULT 127
US-10-027-632-175703/c
; Sequence 175703, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175703
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; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175703

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
Db 9 ATTCGCTGG 1

RESULT 128
US-10-027-632-175703/c
; Sequence 175703, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175703
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175703

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
Db 9 ATTCGCTGG 1

RESULT 129
US-10-027-632-175712/c
; Sequence 175712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175703
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175703

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
Db 9 ATTCGCTGG 1

RESULT 129
US-10-027-632-175712/c
; Sequence 175712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175712
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175712

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
Db 9 ATTCGCTGG 1

RESULT 130
US-10-027-632-175712/c
; Sequence 175712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175712
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175712

Query Match          37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
Db 9 ATTCGCTGG 1

RESULT 131
US-10-314-322-89
; Sequence 89, Application US/10314322
; Publication No. US2003022991A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
```

; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-89

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACTCGCTGG 13
Db 1 ACTGGCTGG 9

RESULT 132
US-10-314-322-177/c
; Sequence 177, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-177

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACTCGCTGG 13
Db 11 ACTGGCTGG 3

Search completed: June 8, 2004, 12:30:12
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 12:28:06 ; Search time 0.001 Seconds
(without alignments)
77.840 Million cell updates/sec

Title: US-10-003-919-21

Perfect score: 20

Sequence: 1 ATGGACTCGTGGCAGGCAC 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 178 seqs, 1946 residues

Total number of hits satisfying chosen parameters: 356

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 178 summaries

Database : rni:db.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.2	66.0	20	1	US-09-798-095-15
C 2	13	65.0	18	1	US-09-143-213-59
C 3	11.2	56.0	17	1	US-08-849-021-31
C 4	11.2	56.0	17	1	US-09-866-108A-9914
C 5	11.2	56.0	17	1	US-09-866-108A-9915
C 6	10.4	52.0	15	1	US-09-081-646-637
C 7	10.4	52.0	16	1	US-09-371-772B-5820
C 8	10.2	51.0	15	1	US-09-176-320-2
C 9	10.2	51.0	15	1	US-09-474-432B-143
C 10	10.2	51.0	15	1	US-09-476-387-143
C 11	10	50.0	15	1	US-08-363-240A-132
C 12	9.8	49.0	15	1	US-08-363-240A-23
C 13	9.8	49.0	15	1	US-08-872-417B-3
C 14	9.8	49.0	15	1	US-09-436-518-3
C 15	9.8	49.0	15	1	US-08-584-040-8489
C 16	9.8	49.0	15	1	US-09-371-772B-4143
C 17	9.4	47.0	14	1	US-09-547-34A-34
C 18	9	45.0	12	1	US-08-929-856-3
C 19	9	45.0	12	1	US-08-929-856-4
C 20	9	45.0	13	1	US-08-574-396-44
C 21	9	45.0	13	1	US-08-544-381B-23
C 22	9	45.0	13	1	US-09-156-828B-14
C 23	9	45.0	13	1	US-08-973-568-44
C 24	9	45.0	13	1	US-08-778-794A-81
C 25	9	45.0	13	1	US-09-306-653-28
C 26	9	45.0	13	1	US-09-306-653-30
C 27	9	45.0	13	1	US-09-306-653-34
C 28	9	45.0	13	1	US-09-306-653-36
C 29	9	45.0	13	1	US-09-306-653-42
C 30	9	45.0	13	1	US-09-306-653-44
C 31	9	45.0	13	1	US-09-621-275-39
C 32	9	45.0	13	1	US-09-621-275-41
C 33	9	45.0	13	1	US-09-621-275-45

1	US-09-621-275-47	13	45.0	9	C 34	Sequence 47, Appl
1	US-09-621-275-53	13	45.0	9	C 35	Sequence 53, Appl
1	US-09-621-275-55	13	45.0	9	C 36	Sequence 55, Appl
1	US-08-547-214-18	12	44.0	8.8	C 37	Sequence 18, Appl
1	US-08-547-214-20	38	44.0	8.8	C 38	Sequence 20, Appl
1	US-08-663-823B-18	39	44.0	8.8	C 39	Sequence 18, Appl
1	US-08-663-823B-20	40	44.0	8.8	C 40	Sequence 20, Appl
1	US-08-942-406-18	41	44.0	8.8	C 41	Sequence 18, Appl
1	US-08-942-406-20	42	44.0	8.8	C 42	Sequence 20, Appl
1	US-09-322-617-18	43	44.0	8.8	C 43	Sequence 18, Appl
1	US-09-322-617-20	44	44.0	8.8	C 44	Sequence 20, Appl
1	US-09-203-231B-22	45	44.0	8.8	C 45	Sequence 22, Appl
1	US-09-203-231B-24	46	44.0	8.8	C 46	Sequence 24, Appl
1	US-09-751-561-18	47	44.0	8.8	C 47	Sequence 18, Appl
1	US-09-751-561-20	48	44.0	8.8	C 48	Sequence 20, Appl
1	US-09-724-385-18	49	44.0	8.8	C 49	Sequence 18, Appl
1	US-09-724-385-20	50	44.0	8.8	C 50	Sequence 20, Appl
1	US-09-757-528-18	51	44.0	8.8	C 51	Sequence 18, Appl
1	US-09-757-528-20	52	44.0	8.8	C 52	Sequence 20, Appl
1	US-08-480-473B-25	53	41.0	8.2	C 53	Sequence 25, Appl
1	US-08-915-213-25	54	41.0	8.2	C 54	Sequence 25, Appl
1	US-09-235-217-25	55	41.0	8.2	C 55	Sequence 25, Appl
1	PCT-US96-10251-25	56	41.0	8.2	C 56	Sequence 25, Appl
1	US-08-859-954-179	57	40.0	8	C 57	Sequence 179, Appl
1	US-08-171-385-28	58	40.0	8	C 58	Sequence 28, Appl
1	US-08-351-748-13	59	40.0	8	C 59	Sequence 13, Appl
1	US-08-430-536A-13	60	40.0	8	C 60	Sequence 13, Appl
1	US-08-463-660-14	61	40.0	8	C 61	Sequence 14, Appl
1	US-08-578-280-14	62	40.0	8	C 62	Sequence 14, Appl
1	US-08-582-261A-4	63	40.0	8	C 63	Sequence 4, Appl
1	US-08-684-547-13	64	40.0	8	C 64	Sequence 13, Appl
1	US-08-942-819-3	65	40.0	8	C 65	Sequence 3, Appl
1	US-08-361-441B-28	66	40.0	8	C 66	Sequence 28, Appl
1	US-09-016-540-4	67	40.0	8	C 67	Sequence 4, Appl
1	US-09-398-499-55	68	40.0	8	C 68	Sequence 55, Appl
1	US-09-308-984-3	69	40.0	8	C 69	Sequence 3, Appl
1	US-09-313-221A-132	70	40.0	8	C 70	Sequence 132, Appl
1	US-09-522-955A-3	71	40.0	8	C 71	Sequence 3, Appl
1	PCT-US93-02246-13	72	40.0	8	C 72	Sequence 13, Appl
1	US-08-327-525A-39	73	40.0	8	C 73	Sequence 39, Appl
1	US-08-531-137B-39	74	40.0	8	C 74	Sequence 39, Appl
1	US-09-158-765-39	75	40.0	8	C 75	Sequence 39, Appl
1	US-09-249-155A-312	76	40.0	8	C 76	Sequence 312, Appl
1	US-09-796-071-39	77	40.0	8	C 77	Sequence 39, Appl
1	US-08-929-856-5	78	40.0	8	C 78	Sequence 5, Appl
1	US-08-152-955-4	79	39.0	7.8	C 79	Sequence 4, Appl
1	PCT-US93-05669-4	80	39.0	7.8	C 80	Sequence 4, Appl
1	US-08-874-825-78	81	39.0	7.8	C 81	Sequence 78, Appl
1	US-08-874-825-79	82	39.0	7.8	C 82	Sequence 79, Appl
1	US-08-663-824-78	83	39.0	7.8	C 83	Sequence 78, Appl
1	US-08-663-824-79	84	39.0	7.8	C 84	Sequence 79, Appl
1	US-09-431-149-32	85	39.0	7.8	C 85	Sequence 32, Appl
1	US-09-231-303-78	86	39.0	7.8	C 86	Sequence 78, Appl
1	US-09-231-303-79	87	39.0	7.8	C 87	Sequence 79, Appl
1	US-09-989-789-2216	88	37.0	7.4	C 88	Sequence 2216, Appl
1	US-09-989-789-2286	89	37.0	7.4	C 89	Sequence 2286, Appl
1	US-08-989-789-2287	90	37.0	7.4	C 90	Sequence 2287, Appl
1	US-08-170-290A-1	91	37.0	7.4	C 91	Sequence 1, Appl
1	US-08-309-245-1	92	37.0	7.4	C 92	Sequence 1, Appl
1	US-08-462-389-1	93	37.0	7.4	C 93	Sequence 1, Appl
1	US-07-724-500B-4	94	37.0	7.4	C 94	Sequence 4, Appl
1	US-08-463-101-1	95	37.0	7.4	C 95	Sequence 1, Appl
1	US-08-618-700-1	96	37.0	7.4	C 96	Sequence 1, Appl
1	US-08-451-418B-4	97	37.0	7.4	C 97	Sequence 4, Appl
1	US-08-451-418B-21	98	37.0	7.4	C 98	Sequence 21, Appl
1	US-08-477-504A-21	99	37.0	7.4	C 99	Sequence 21, Appl
1	US-08-486-756A-21	100	37.0	7.4	C 100	Sequence 21, Appl
1	US-08-485-862B-21	101	37.0	7.4	C 101	Sequence 21, Appl
1	US-08-388-353-703	102	37.0	7.4	C 102	Sequence 703, Appl
1	US-08-388-353-704	103	37.0	7.4	C 103	Sequence 704, Appl
1	US-08-388-353-769	104	37.0	7.4	C 104	Sequence 769, Appl
1	US-08-388-353-770	105	37.0	7.4	C 105	Sequence 770, Appl
1	US-08-388-353-770	106	37.0	7.4	C 106	Sequence 770, Appl

107	7.4	37.0	10	1	US-08-488-551B-703	Sequence 703, App
108	7.4	37.0	10	1	US-08-488-551B-704	Sequence 704, App
109	7.4	37.0	10	1	US-08-488-551B-769	Sequence 769, App
110	7.4	37.0	10	1	US-08-488-551B-770	Sequence 770, App
111	7.4	37.0	10	1	US-08-793-398-1	Sequence 1, Appli
112	7.4	37.0	10	1	US-09-157-601-1	Sequence 1, Appli
113	7.4	37.0	10	1	US-08-487-077A-21	Sequence 21, Appl
114	7.4	37.0	10	1	US-08-485-863A-21	Sequence 21, Appl
115	7.4	37.0	10	1	US-08-485-049D-21	Sequence 21, Appl
116	7.4	37.0	10	1	US-08-899-241-240	Sequence 240, App
117	7.4	37.0	10	1	US-09-235-899-4	Sequence 4, Appli
118	7.4	37.0	10	1	US-09-989-789-367	Sequence 367, App
119	7.4	37.0	10	1	US-09-989-789-568	Sequence 568, App
120	7.4	37.0	10	1	PCT-US91-01822A-4	Sequence 4, Appli
121	7.4	37.0	10	1	PCT-US91-02628-4	Sequence 4, Appli
122	7.4	37.0	10	1	PCT-US95-11982-1	Sequence 1, Appli
123	7.4	37.0	10	1	PCT-US95-11982A-1	Sequence 1, Appli
124	7.4	37.0	11	1	US-09-249-155A-89	Sequence 89, Appli
125	7.4	37.0	11	1	US-09-249-155A-177	Sequence 177, App
126	7.4	37.0	8	1	US-08-480-173A-18	Sequence 18, Appl
127	7.4	37.0	8	1	US-08-859-954-148	Sequence 148, App
128	7.4	37.0	8	1	US-08-484-408A-18	Sequence 18, Appl
129	7.4	37.0	8	1	US-09-398-499-1	Sequence 1, Appli
130	7.4	37.0	8	1	US-09-398-499-6	Sequence 6, Appli
131	7.4	37.0	8	1	US-09-398-499-24	Sequence 24, Appli
132	7.4	37.0	8	1	US-09-398-499-29	Sequence 29, Appli
133	7.4	37.0	9	1	US-08-362-495-3	Sequence 3, Appli
134	7.4	37.0	9	1	US-09-989-789-2378	Sequence 2378, Ap
135	7.4	37.0	10	1	US-09-398-499-53	Sequence 53, Appl
136	7.4	37.0	10	1	US-09-154-750A-41	Sequence 41, Appl
137	7.4	37.0	10	1	US-09-475-947A-182	Sequence 182, App
138	7.4	37.0	10	1	US-09-763-482-33	Sequence 33, Appl
139	6.8	34.0	10	1	US-08-750-655-1	Sequence 1, Appli
140	6.8	34.0	10	1	US-08-388-353-669	Sequence 669, App
141	6.8	34.0	10	1	US-08-388-353-670	Sequence 670, App
142	6.8	34.0	10	1	US-08-388-353-771	Sequence 771, App
143	6.8	34.0	10	1	US-08-488-551B-669	Sequence 669, App
144	6.8	34.0	10	1	US-08-488-551B-670	Sequence 670, App
145	6.8	34.0	10	1	US-08-488-551B-771	Sequence 771, App
146	6.8	34.0	10	1	US-08-757-024-864	Sequence 864, App
147	6.8	34.0	10	1	US-08-297-395-59	Sequence 59, Appl
148	6.8	34.0	10	1	US-08-878-835A-6	Sequence 6, Appli
149	6.8	34.0	10	1	US-09-508-753B-195	Sequence 195, App
150	6.8	34.0	10	1	US-09-508-753B-289	Sequence 289, App
151	6.8	34.0	10	1	US-09-508-753B-387	Sequence 387, App
152	6.8	34.0	10	1	US-09-508-753B-389	Sequence 389, App
153	6.8	34.0	10	1	US-08-894-454-132	Sequence 132, App
154	6.8	34.0	10	1	US-09-769-482-49	Sequence 49, Appl
155	6.8	34.0	10	1	US-09-989-789-1268	Sequence 1268, Ap
156	6.4	32.0	8	1	US-08-232-144-10	Sequence 10, Appl
157	6.4	32.0	8	1	US-08-859-954-178	Sequence 178, App
158	6.4	32.0	8	1	US-08-859-954-202	Sequence 202, App
159	6.4	32.0	8	1	US-08-859-954-210	Sequence 210, App
160	6.4	32.0	8	1	US-08-859-954-212	Sequence 212, App
161	6.4	32.0	8	1	US-08-859-954-213	Sequence 213, App
162	6.4	32.0	8	1	US-08-859-954-403	Sequence 403, App
163	6.4	32.0	8	1	US-09-398-499-8	Sequence 8, Appli
164	6.4	32.0	8	1	US-09-398-499-16	Sequence 16, Appl
165	6.4	32.0	8	1	US-09-398-499-31	Sequence 31, Appl
166	6.4	32.0	8	1	US-09-398-499-39	Sequence 39, Appl
167	6.4	32.0	9	1	US-08-488-015B-9	Sequence 9, Appli
168	6.4	32.0	9	1	US-08-717-536-61	Sequence 61, Appl
169	6.4	32.0	9	1	US-08-360-051A-46	Sequence 46, Appl
170	6.4	32.0	9	1	US-08-796-899-17	Sequence 17, Appl
171	6.4	32.0	9	1	US-09-034-205-48	Sequence 48, Appl
172	6.4	32.0	9	1	US-08-934-097A-48	Sequence 48, Appl
173	6.4	32.0	9	1	US-09-677-218B-48	Sequence 48, Appl
174	6.4	32.0	9	1	US-09-677-132-48	Sequence 48, Appl
175	6.4	32.0	9	1	US-09-380-836-4	Sequence 4, Appli
176	6.4	32.0	9	1	US-09-989-789-2195	Sequence 2195, Ap
177	6.4	32.0	9	1	US-09-958-221A-7	Sequence 7, Appli
178	6.4	32.0	9	1	PCT-US96-01008-2	Sequence 2, Appli

ALIGNMENTS

```

RESULT 1
US-09-798-096-15/c
; Sequence 15, Application US/09798096
; Patent No. 6393378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-798-096-15

Query Match          66.0%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 7;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGGACTCGCTGGCAGCA 19
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Db      18 TGGCTTGTATGGCAGCA 1

RESULT 2
US-09-143-212-59/c
; Sequence 59, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-59

Query Match          65.0%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGGACTCGCTGGC 14
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Db      18 TGGACTCGCTGGC 6

RESULT 3
US-08-849-021-31/c
; Sequence 31, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
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Query Match 56.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGGCAC 16
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Db 16 AGGACTCGCAGGAAC 1

RESULT 6
US-09-081-646-637
; Sequence 637, Application US/09081646
; Patent No. 633352
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 637
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-637

Query Match 52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTG 12
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Db 2 ATGGACTCTCTG 13

RESULT 7
US-09-371-772B-5820/c
; Sequence 5820, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5820
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5820

Query Match 52.0%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
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Db 16 GTACTCGCTGGC 5

RESULT 8
US-09-176-320-2/c
; Sequence 2, Application US/09176320
; Patent No. 617281
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Jacobs, Henk
; TITLE OF INVENTION: PREVENTION OF BT RESISTANCE DEVELOPMENT
; FILE REFERENCE: 021565-052
; CURRENT APPLICATION NUMBER: US/09/176,320
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: PCT/EP90/00905
; EARLIER FILING DATE: 1990-05-30
; EARLIER APPLICATION NUMBER: GB 89401499.2
; EARLIER FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-176-320-2

Query Match 51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGGCA 15
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Db 15 ATGGTGGCGCTGGCA 1

RESULT 9
US-09-474-432B-143
; Sequence 143, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-143

Query Match 51.0%; Score 10.2; DB 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 16
:|||||:|||||
Db 1 UGAGCGCGUGAC 15

RESULT 10
US-09-476-387-143
; Sequence 143, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MBH00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-143

Query Match 51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 16
:|||||:|||||
Db 1 UGAGCGCGUGAC 15

RESULT 11
US-08-363-240A-132
; Sequence 132, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pace, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 210/096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-240A-23

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 27;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CTCGCTGGCAGGC 18
 |||||
 Db 15 CTCGCTGGAGGC 3

RESULT 13
 US-08-872-417B-3
 ; Sequence 3, Application US/08872417B
 ; Patent No. 6066470
 ; GENERAL INFORMATION:
 ; APPLICANT: Nishimura, Osamu
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Ohmae, Hiroaki
 ; APPLICANT: Teuji, Shinji
 ; TITLE OF INVENTION: Method of Removing N-terminal
 ; TITLE OF INVENTION: Methionine
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/872,417B
 ; FILING DATE: 10-JUN-1997
 ; CLASSIFICATION: 5.4
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JA 154634/96
 ; FILING DATE: 14-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 47423
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-872-417B-3

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 27;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TCCCTGGCAGCA 19
 |||||
 Db 3 TCCCTGGCATGCA 15

RESULT 14
 US-09-436-518-3
 ; Sequence 3, Application US/09436518
 ; Patent No. 6309859
 ; GENERAL INFORMATION:
 ; APPLICANT: NISHIMURA, OSAMU
 ; APPLICANT: SUENAGA, MASATO
 ; APPLICANT: OHMAE, HIROAKI
 ; APPLICANT: TSUJI, SHINJI
 ; TITLE OF INVENTION: METHOD FOR REMOVING N-TERMINAL METHIONINE
 ; FILE REFERENCE: 47423-CPA-CON (342)
 ; CURRENT APPLICATION NUMBER: US/09/436,518
 ; CURRENT FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 08/872,417
 ; PRIOR FILING DATE: 1997-06-10
 ; PRIOR APPLICATION NUMBER: JP 8-154634
 ; PRIOR FILING DATE: 1996-06-14
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: adapter
 ; US-09-436-518-3

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 27;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TCCCTGGCAGCA 19
 |||||
 Db 3 TCCCTGGCATGCA 15

RESULT 15
 US-08-584-040-8489
 ; Sequence 8489, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 ; TITLE OF INVENTION: GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 8502
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:

```

/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,337
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 8489:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-8489

```

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGG 13
| : | | : | : | : |
Db 1 AUGGAAUCUCUGG 13

```

RESULT 16
US-09-371-772B-4143
/ Sequence 4143, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for
/ TITLE OF INVENTION: Levels of Vascular En
/ FILE REFERENCE: MBH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371.772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 09/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4143
/ LENGTH: 15
/ TYPE: RNA
/ ORGANISM: Mus sp.
US-09-371-772B-4143

```

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. NO. 27;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGG 13
| : | | : | : | : |
Db 1 AUGGAAUCUCUGG 13

RESULT 17
US-09-647-344A-34
; Sequence 34, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.

```

; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 34
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-647-344A-34

Query Match          47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 72.7%; Pred.No.30;
Matches 8; Conservative 2; Mismatches 1; Indels

QY      3  GGACTCGCTGG 13
      |||  |||  |||
DB      3  GGAUUCGUG 13

RESULT 18
US-08-929-856-3
; Sequence 3, Application US/08929856
; Patent No. 6136568
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Rose, Floyd
; TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
; TITLE OF INVENTION: ROLLING TEMPLATES
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/929,856
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: ROSE 3.0-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-929-856-3

```

```
Query Match          45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 ATGGACTCG 9

Db 3 ATGGACTCG 11

RESULT 19
US-08-929-856-4
; Sequence 4, Application US/08929856
; Patent No. 6136588
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Rose, Floyd
; TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
; TITLE OF INVENTION: ROLLING TEMPLATES
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: ROSE 3.0-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-929-856-4

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
|||||
Db 4 ATGGACTCG 12

RESULT 20
US-08-574-396-44/c
; Sequence 44, Application US/08574396
; Patent No. 6001648
; GENERAL INFORMATION:
; APPLICANT: McCall, Maxine J.
; APPLICANT: Hendry, Philip
; APPLICANT: Lockett, Trevor
; TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
|||||
Db 4 ATGGACTCG 12

RESULT 21
US-08-544-381B-23/c
; Sequence 23, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Ches, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xishua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305

Qy 2 TGGACTCGC 10
|||||
Db 9 TGGACTCGC 1

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGACTCGC 10
|||||
Db 9 TGGACTCGC 1

US-08-574-396-44

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,396
FILING DATE: 18-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1012/47203-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278-0400
TELEFAX: 212 391-0525
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-00413005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-23

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 11 GGCACGCAC 3

RESULT 22
US-09-156-828B-14/c
; Sequence 14, Application US/09156828B
; Patent No. 6238917
; GENERAL INFORMATION:
; APPLICANT: Hendry, Philip
; APPLICANT: McCall, Maxine J.
; TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZYMES
; FILE REFERENCE: 50534bpu
; CURRENT APPLICATION NUMBER: US/09/156,828B
; CURRENT FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/AU97/00210
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RIBOZYMES AND PORTIONS THEREOF
US-09-156-828B-14

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTCGC 10
Db 9 TGGACTCGC 1

RESULT 23
US-08-973-568-44/c
; Sequence 44, Application US/08973568B
; Patent No. 6277534
; GENERAL INFORMATION:
; APPLICANT: McCall, Maxine J.
; APPLICANT: Hendry, Philip
; APPLICANT: Lockett, Trevor
; TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF

; FILE REFERENCE: 47203bpctus
; CURRENT APPLICATION NUMBER: US/08/973,568B
; CURRENT FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Ribozyme or portion thereof
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
; OTHER INFORMATION: portions thereof
US-08-973-568-44

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTCGC 10
Db 9 TGGACTCGC 1

RESULT 24
US-08-778-794A-81/c
; Sequence 81, Application US/08778794A
; Patent No. 6309823
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, MacDonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes
; TITLE OF INVENTION: for Analyzing Biotransformation Genes
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,794A
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: US 08/544,381
; FILING DATE: 10-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 018547-015700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEX:
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-778-794A-81

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCAGGCAC 20
Db 11 GGCAGGCAC 3

RESULT 25
US-09-306-653-28/c
Sequence 28, Application US/09306653
Patent No. 6600026
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia C.
APPLICANT: Yu, Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Utilizing Monolayers
FILE REFERENCE: A66343-1/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/306,653
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/084,652
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 09/135,183
EARLIER FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-306-653-28

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2

RESULT 26
US-09-306-653-30/c
Sequence 30, Application US/09306653
Patent No. 6600026
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia C.
APPLICANT: Yu, Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Utilizing Monolayers
FILE REFERENCE: A66343-1/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/306,653
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/084,652

EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 09/135,183
EARLIER FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-306-653-30

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2

RESULT 27
US-09-306-653-34/c
Sequence 34, Application US/09306653
Patent No. 6600026
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia C.
APPLICANT: Yu, Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Utilizing Monolayers
FILE REFERENCE: A66343-1/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/306,653
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/084,652
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 09/135,183
EARLIER FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-306-653-34

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2

RESULT 28
US-09-306-653-36/c
Sequence 36, Application US/09306653
Patent No. 6600026
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia C.
APPLICANT: Yu, Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Utilizing Monolayers
FILE REFERENCE: A66343-1/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/306,653
CURRENT FILING DATE: 1999-05-06

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;

QY 1 ATGGACTCG 9
|||
Db 10 ATGGACTCG 2

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; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39

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;
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: De

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Qy 1 ATGGACTCG 9
|||
Db 10 ATGGACTCG 2

RESULT 32

US-09-621-275-41/c
; Sequence 41, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-41

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||
Db 10 ATGGACTCG 2

RESULT 33
US-09-621-275-45/c
; Sequence 45, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-45

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||
Db 10 ATGGACTCG 2

RESULT 34
US-09-621-275-47/c
; Sequence 47, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-47

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||
Db 10 ATGGACTCG 2

RESULT 35
US-09-621-275-53/c
; Sequence 53, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RFT/RMS/RMK

; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60,084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-53

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
| | | | |
Db 10 ATGGACTCG 2

RESULT 36
US-09-621-275-55/c
; Sequence 55, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: APPLICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RET/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60,084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-55

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
| | | | |
Db 10 ATGGACTCG 2
RESULT 37
US-08-547-214-18
; Sequence 18, Application US/08547214
; Patent No. 5871697
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/547,214
; FILING DATE: 24-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-547-214-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
| | | | |
Db 1 AGTCGCTGGTAC 12

RESULT 38
US-08-547-214-20
; Sequence 20, Application US/08547214
; Patent No. 5871697
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and

```
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
;
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/547,214
; FILING DATE: 24-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-547-214-20
;
; Query Match 44.0%; Score 8.8; DB 1; Length 12;
; Best Local Similarity 83.3%; Pred. No. 34;
; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 5 ACTCGCTGGCAC 16
; Db 1 AGTCGCTGGTAC 12
;
; RESULT 39
; US-08-663-823B-18
; Sequence 18, Application US/08663823B
; Patent No. 5972693
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
; TITLE OF INVENTION: CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
; TITLE OF INVENTION: WITHOUT SEQUENCING
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,823B
; FILING DATE: 14-June-1996
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-663-823B-20
;
; Query Match 44.0%; Score 8.8; DB 1; Length 12;
; Best Local Similarity 83.3%; Pred. No. 34;
; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 5 ACTCGCTGGCAC 16
; Db 1 AGTCGCTGGCGC 12
;
; RESULT 39
; US-08-663-823B-18
; Sequence 18, Application US/08663823B
; Patent No. 5972693
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
; TITLE OF INVENTION: CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
; TITLE OF INVENTION: WITHOUT SEQUENCING
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,823B
; FILING DATE: 14-June-1996
; CLASSIFICATION: 422
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-663-823B-18
;
; Query Match 44.0%; Score 8.8; DB 1; Length 12;
; Best Local Similarity 83.3%; Pred. No. 34;
; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 5 ACTCGCTGGCAC 16
; Db 1 AGTCGCTGGTAC 12
;
; RESULT 40
; US-08-663-823B-20
; Sequence 20, Application US/08663823B
; Patent No. 5972693
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
; TITLE OF INVENTION: CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
; TITLE OF INVENTION: WITHOUT SEQUENCING
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,823B
; FILING DATE: 14-June-1996
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-663-823B-20
;
; Query Match 44.0%; Score 8.8; DB 1; Length 12;
; Best Local Similarity 83.3%; Pred. No. 34;
```

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGCGC 12

RESULT 41

US-08-942-406-18
; Sequence 18, Application US/08942406
; Patent No. 6141657
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,406
; FILING DATE: 01-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; INFORMATION FOR SEQ ID NO: 18:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-942-406-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 42

US-08-942-406-20
; Sequence 20, Application US/08942406
; Patent No. 6141657
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,406
; FILING DATE: 01-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; INFORMATION FOR SEQ ID NO: 20:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-942-406-20

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGCGC 12

RESULT 43

US-09-322-617-18
; Sequence 18, Application US/09322617
; Patent No. 6231812
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,617
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; PENTEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-322-617-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 44
US-09-322-617-20
; Sequence 20, Application US/09322617
; Patent No. 6231812
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,617
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; PENTEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-322-617-20

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGGCG 12

RESULT 45
US-09-203-231B-22
; Sequence 22, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-22

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 46
US-09-203-231B-24
; Sequence 24, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-24

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Query Match      44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGCC 12

RESULT 47
US-09-751-561-18
; Sequence 19, Application US/09751561
; Patent No. 6418382
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-751-561-18

Query Match      44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12

RESULT 48
US-09-751-561-20
; Sequence 20, Application US/09751561
; Patent No. 6418382
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
```

```
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Determination and
TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,561
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/547,214
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-790-9090
TELEFAX: (212)-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-751-561-20

Query Match      44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGCC 12

RESULT 49
US-09-724-385-18
; Sequence 18, Application US/09724385
; Patent No. 6432361
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/724,385
; FILING DATE: 28-No. 6432361-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/322,617
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-724-385-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
DB 1 AGTCGCTGGTAC 12

RESULT 50
US-09-724-385-20
; Sequence 20, Application US/09724385
; Patent No. 6432361
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,385
; FILING DATE: 28-No. 6432361-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/322,617
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-757-528-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
DB 1 AGTCGCTGGTAC 12

RESULT 51
US-09-757-528-18
; Sequence 18, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,528
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-757-528-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
DB 1 AGTCGCTGGTAC 12

RESULT 52
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-724-385-20

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
DB 1 AGTCGCTGGC 12

RESULT 51
US-09-757-528-18
; Sequence 18, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,528
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-757-528-18

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
DB 1 AGTCGCTGGTAC 12

RESULT 52
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US-09-757-528-20
; Sequence 20, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09757,528
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-757-528-20
Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTGCTGGGCAC 16
Db 1 AGTCGCTGGGCC 12

RESULT 53
US-08-480-473B-25/c
; Sequence 25, Application US/08480473B
; Patent No. 5882314
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; COMPUTER: IBM PC compatible

US-09-757-528-20
Query Match 41.0%; Score 8.2; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGGCAC 20
Db 12 TSKCAGCNC 3

RESULT 54
US-08-915-213-25/c
; Sequence 25, Application US/08915213
; Patent No. 6020462
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,213
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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Tue Jun 8 12:32:43 2004

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; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: N is inosine.
US-08-915-213-25
Query Match 41.0%; Score 8.2; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
Db 12 TSKCAGGCNC 3

RESULT 55
US-09-235-217-25/c
; Sequence 25, Application US/09235217
; Patent No. 6222018
; GENERAL INFORMATION:
; APPLICANT: Senenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,217
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,473
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: N is inosine.
US-09-235-217-25
Query Match 41.0%; Score 8.2; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
Db 12 TSKCAGGCNC 3

RESULT 56
PCT-US96-10251-25/c
; Sequence 25, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
```

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; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10251
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: N is inosine.
PCT-US96-10251-25
Query Match 41.0%; Score 8.2; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
Db 12 TSKCAGGCNC 3

RESULT 57
US-08-859-954-179/c
; Sequence 179, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-179

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
Db 8 ATGGACTC 1

RESULT 58
US-08-171-385-28/c
; Sequence 28, Application US/08171385
; Patent No. 5527884
; GENERAL INFORMATION:
; APPLICANT: Mary E. Russell
; APPLICANT: Ulrike Utans
; TITLE OF INVENTION: Mediators of Chronic Allograft
; TITLE OF INVENTION: Rejection
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,385
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/006001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-171-385-28

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 59
US-08-351-748-13/c
; Sequence 13, Application US/08351748
; Patent No. 559672
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; APPLICANT: Pardee, Arthur B.
; APPLICANT: Bianchi, Cesario F.
; TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
; TITLE OF INVENTION: MESSENGER RNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,748
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,084
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 181411-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-351-748-13

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 60
US-08-430-536A-13/c
; Sequence 13, Application US/08430536A
; Patent No. 566547
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; APPLICANT: Liang, Peng
```

```

; APPLICANT: Pardee, Arthur B.
; TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
; TITLE OF INVENTION: MESSENGER RNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,536A
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herschbach Ph.D., Brenda M.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 181411-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-430-536A-13

```

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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

```

```

RESULT 61
US-08-463-660-14/c
; Sequence 14, Application US/08463660
; Patent No. 5759776
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,660
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.

```

```

; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 28888-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-660-14

```

```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

```

```

RESULT 62
US-08-678-280-14/c
; Sequence 14, Application US/08678280
; Patent No. 5776683
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,280
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 28888-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-678-280-14

```

```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

```

```

RESULT 63
US-08-582-261A-4/c
; Sequence 4, Application US/08582261A
; Patent No. 5817461
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard C.
; APPLICANT: Hirsch, Jack
; APPLICANT: Weitz, Jeff
; TITLE OF INVENTION: Methods and Compositions for Diagnosis
; TITLE OF INVENTION: of Hyperhomocysteinemia
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,261A
; FILING DATE: 03-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 016558-001200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-582-261A-4

```

```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 TCGCTGGC 14
    |||||
Db 9 TCGCTGGC 2

```

```

RESULT 64
US-08-684-547-13/c
; Sequence 13, Application US/08684547
; Patent No. 5965409
; GENERAL INFORMATION:
; APPLICANT: Pardee Ph.D., Arthur B.
; APPLICANT: Liang Ph.D., Peng
; TITLE OF INVENTION: SYSTEM FOR COMPARING LEVELS OR AMOUNTS
; TITLE OF INVENTION: OF mRNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,547
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0181411-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-684-547-13

```

```

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 TCGCTGGC 14
    |||||
Db 9 TCGCTGGC 2

```

```

RESULT 65
US-08-942-819-3/c
; Sequence 3, Application US/08942819
; Patent No. 5965707
; GENERAL INFORMATION:
; APPLICANT: Tam, See-Ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF
; TITLE OF INVENTION: RAS-MEDIATED SIGNALING
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,819
; FILING DATE: 02-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/058,520
; FILING DATE: 11-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BIH96-13pa
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-942-819-3

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TCGCTGGC 14
Db      9 TCGCTGGC 2

RESULT 66
US-08-361-441B-28/c
; Sequence 28, Application US/08361441B
; Patent No. 6077948
; GENERAL INFORMATION:
; APPLICANT: Russell, Mary E.
; APPLICANT: Utans, Urike
; TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,441B
; FILING DATE: 21-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/171,385
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-361-441B-28

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TCGCTGGC 14
Db      9 TCGCTGGC 2

RESULT 67
US-09-016-540-4/c
; Sequence 4, Application US/09016540
; Patent No. 6132965
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard C.
; APPLICANT: Hirsh, Jack
```

```
; APPLICANT: Weitz, Jeff
; TITLE OF INVENTION: Methods and Compositions for Diagnosis
; TITLE OF INVENTION: of Hyperhomocysteinemia
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,261
; FILING DATE: 03-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 016558-001200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-016-540-4

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TCGCTGGC 14
Db      9 TCGCTGGC 2

RESULT 68
US-09-398-499-55/c
; Sequence 55, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-55

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 8 CGCTGGCA 15
Db 9 CGCTGGCA 2

RESULT 69

US-09-308-984-3/c
; Sequence 3, Application US/09308984

; Patent No. 6388065

; GENERAL INFORMATION:

; APPLICANT: Durst, Matthias

; APPLICANT: Nees, Matthias

; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS

; FILE REFERENCE: SCHU 204 (09902857)

; CURRENT APPLICATION NUMBER: US/09/308,984

; PRIOR FILING DATE: 1999-09-03

; PRIOR APPLICATION NUMBER: PCT/DE97/02660

; PRIOR FILING DATE: 1996-11-12

; PRIOR APPLICATION NUMBER: DE 196 49207

; PRIOR FILING DATE: 1997-11-27

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 3

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-308-984-3

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 70

US-09-313-221A-132/c

; Sequence 132, Application US/09313221A

; Patent No. 6468743

; GENERAL INFORMATION:

; APPLICANT: Thomas L. Romick (Inventor)

; APPLICANT: Mark S. Fraser (Inventor)

; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL

; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS

; FILE REFERENCE: HUNT-042784

; CURRENT APPLICATION NUMBER: US/09/313,221A

; CURRENT FILING DATE: 1999-05-17

; PRIOR APPLICATION NUMBER: US 60/086,025

; PRIOR FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 132

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Compylobacter jejuni

US-09-313-221A-132

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 71

US-09-522-955A-3/c

; Sequence 3, Application US/09522955A

; Patent No. 6500942

; GENERAL INFORMATION:

; APPLICANT: Tam, See-Ying

; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF RAS-MEDICATED
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 1440.1089-004
; CURRENT APPLICATION NUMBER: US/09/522,955A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19056
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/942,819
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: US 60/058,520
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-522-955A-3

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 72

PCT-US93-02246-13/c

; Sequence 13, Application PC/TUS9302246

; GENERAL INFORMATION:

; APPLICANT: Liang, Peng

; APPLICANT: Pardee, Arthur B.

; TITLE OF INVENTION: Identifying, Isolating and Cloning

; TITLE OF INVENTION: Messenger RNAs

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Choate, Hall & Stewart

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02190

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/02246

; FILING DATE: 19930311

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/850,343

; FILING DATE: 11-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pasternack, Sam

; REGISTRATION NUMBER: 29,576

; REFERENCE/DOCKET NUMBER: DFCI234CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617 227-5020

; TELEFAX: 617 227-7566

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

```
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-02246-13

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 73
US-08-327-525A-39
; Sequence 39, Application US/08327525A
; Patent No. 5795716
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; ADDRESSEE: Wang, Chunwei
; APPLICANT: Jevons, Luis C.
; APPLICANT: Bernhart, Derek H.
; APPLICANT: Lipschutz, Robert J.
; TITLE OF INVENTION: Computer-Aided Visualization and
; ANALYSIS SYSTEM FOR SEQUENCE EVALUATION
; Patent No. 5795716
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,525A
; FILING DATE: October 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5795716v1el, Vernon A.
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528X-82
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-327-525A-39

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 74
US-08-531-137B-39
; Sequence 39, Application US/08531137B
; Patent No. 5974164
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; ANALYSIS SYSTEM FOR SEQUENCE EVALUATION
; Patent No. 5974164
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-531-137B-39

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 75
US-09-158-765-39
; Sequence 39, Application US/09158765
; Patent No. 6242180
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; ANALYSIS SYSTEM FOR SEQUENCE EVALUATION
; Patent No. 6242180
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,137
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: APTYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-09-158-765-39

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 76
US-09-249-155A-312/c
; Sequence 312, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-249-155A-312

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGCACGCA 19
Db 11 GGCACGCA 4

RESULT 77
US-09-796-071-39
; Sequence 39, Application US/09796071
; Patent No. 6607887
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; Analysis System for Sequence Evaluation
; Patent No. 6607887
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/796,071
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,137
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: APTYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
; US-09-796-071-39

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 78
US-08-929-856-5
; Sequence 5, Application US/08929856
; Patent No. 6136568
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Rose, Floyd
; TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
; ROLLING TEMPLATES
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; MENTLIK
; ADDRESS: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.

```

REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: ROSE 3.0-057
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-929-856-5

Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
Db 5 ATGGACTC 12

RESULT 79
US-08-152-955-4/c
Sequence 4, Application US/08152955
Patent No. 5474897
GENERAL INFORMATION:
APPLICANT: Weiss, Arthur
APPLICANT: Fraser, James
TITLE OF INVENTION: Screening Assay for the Identification
of Immunosuppressive Drugs
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/152.955
CLASSIFICATION: 435
APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/898,639
FILING DATE: 15-JUN-1992
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-356
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-152-955-4

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGACTCGCTG 12
Db 11 TGGAACTCTCG 1

Db 11 TGGAACTCTCG 1

RESULT 80
PCT-US93-05668-4/c
Sequence 4, Application PC/TUS9305668
GENERAL INFORMATION:
APPLICANT: Weiss, Arthur
APPLICANT: Fraser, James
TITLE OF INVENTION: Screening Assay for the Identification
of Immunosuppressive Drugs
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fisher & Amzel
STREET: 1320 Harbor Bay Parkway, Suite 225
CITY: Alameda
STATE: California
COUNTRY: USA
ZIP: 94501

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US93/05668
FILING DATE: 19930611
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,639
FILING DATE: 15-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Stanley P.
REGISTRATION NUMBER: 24,344
REFERENCE/DOCKET NUMBER: 91-143-1PCT
TELEPHONE: 510-748-6868
TELEFAX: 510-748-6888
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-05668-4

Qy 2 TGGACTCGCTG 12
Db 11 TGGAACTCTCG 1

RESULT 81
US-08-874-825-78
Sequence 78, Application US/08874825
Patent No. 6057101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Yang, Meijia
APPLICANT: Knight, James
APPLICANT: Kalbfleisch, Theodore
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
OF INHIBITORS OF THESE INTERACTIONS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,824
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-874-825-78

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 1 TCGAGTCGCTG 11

RESULT 82
US-08-874-825-79
Sequence 79, Application US/08874825
Patent No. 6057101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Yang, Meijia
APPLICANT: Knight, James
APPLICANT: Kalbfleisch, Theodore
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,824
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-874-825-79

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 1 TCGAGTCGCTG 11

RESULT 83
US-08-663-824-78
Sequence 78, Application US/08663824
Patent No. 6083693
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-78

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 1 TCGAGTCGCTG 11

RESULT 84
US-08-663-824-79
Sequence 79, Application US/08663824
Patent No. 6083693
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 79
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-79

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
   ||| ||| |||
DB 1 TCGAGTCGCTG 11

RESULT 85
US-09-281-418-181
; Sequence 181, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 181
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-181

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCA 15
   ||| ||| |||
DB 1 ACTGGCCGGCA 11

RESULT 86
US-09-043-149-32
; Sequence 32, Application US/09043149
; Patent No. 6355418
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Gunter
; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
; TITLE OF INVENTION: Identification of Antisense Binding Sites
; FILE REFERENCE: 020600-272
; CURRENT APPLICATION NUMBER: US/09/043,149
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/GB96/02275
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: GB 9518864.5
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: oligonucleotide
US-09-043-149-32

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGCCAGCA 19
   ||| ||| |||
DB 2 GCTGCCAGCA 12

RESULT 87
US-09-231-303-78
; Sequence 78, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-78

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
   ||| ||| |||
DB 1 TCGAGTCGCTG 11

RESULT 88
US-09-231-303-79
; Sequence 79, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-79

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
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```
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGACTCGCTG 12
   ||| |||||
Db 1 TGCAGTCGCTG 11

RESULT 89
US-09-989-789-2216
; Sequence 2216, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2216
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2216

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
   ||||| |
Db 1 ATGGACTTG 9

RESULT 90
US-09-989-789-2286
; Sequence 2286, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2286
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2286

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
   ||||| |
Db 1 ATGGACTTG 9

RESULT 91
US-09-989-789-2287
; Sequence 2287, Application US/09989789
; Patent No. 6588746
```

```
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2287
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2287

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
   ||||| |
Db 1 ATGGACTTG 9

RESULT 92
US-08-170-290A-1/c
; Sequence 1, Application US/08170290A
; Patent No. 5702931
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Morser, Michael J.
; APPLICANT: Zielesner, Laura R.
; TITLE OF INVENTION: No. 5702931el Mutagenesis Methods and
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James M. Heslin
; STREET: 379 Lytton Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,290A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/724,237
; FILING DATE: 01-JUL-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 11972-58-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-170-290A-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCA 19
||| |||
Db 10 TGGCGGCA 2

RESULT 93
US-08-309-245-1
Sequence 1, Application US/08309245
Patent No. 5723289
GENERAL INFORMATION:
APPLICANT: EATON, B. AND GOLD, L.
TITLE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,245
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-309-245-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
||| |||
Db 2 CAGGCAGC 10

RESULT 94
US-08-462-389-1
Sequence 1, Application US/08462389
Patent No. 5723592
GENERAL INFORMATION:
APPLICANT: Eaton, Bruce
TITLE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite#200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0 (a) For Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-309-245-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
||| |||
Db 2 CAGGCAGC 10

RESULT 95
US-07-724-500B-4
Sequence 4, Application US/07724500B
Patent No. 5736294
GENERAL INFORMATION:
APPLICANT: Ecker et al.
TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING GENE EXPRESSION TH
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5736294ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/724,500B

APPLICANT: Eaton, Bruce
APPLICANT: Gold, Larry
TITLE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite#200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0 (a) For Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX22-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-389-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
||| |||
Db 2 CAGGCAGC 10

RESULT 95
US-07-724-500B-4
Sequence 4, Application US/07724500B
Patent No. 5736294
GENERAL INFORMATION:
APPLICANT: Ecker et al.
TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING GENE EXPRESSION TH
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5736294ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/724,500B


```

; FILING DATE: June 27, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/US91/01822
; APPLICATION NUMBER: 19 March 1991
; FILING DATE: 19 March 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-0309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-07-724-500B-4

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
Db 2 CUCUCUGGC 10

RESULT 96
US-08-463-101-1
; Sequence 1, Application US/08463101
; Patent No. 5789160
; GENERAL INFORMATION:
; APPLICANT: Eaton, Bruce
; TITLE OF INVENTION: PARALLEL SELEX
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite#200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 07/714,131
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,245
; FILING DATE: 20-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX22-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-101-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
Db 2 CAGGCAGC 10

RESULT 97
US-08-618-700-1
; Sequence 1, Application US/08618700
; Patent No. 5856660
; GENERAL INFORMATION:
; APPLICANT: EATON, BRUCE; GOLD, LARRY
; TITLE OF INVENTION: PARALLEL SELEX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,700
; FILING DATE: March 20, 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,245
; FILING DATE: 20-SEPTEMBER-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX22/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-618-700-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
Db 2 CAGGCAGC 10

RESULT 98
US-08-461-418B-4
; Sequence 4, Application US/08461418B
; Patent No. 5874564
; GENERAL INFORMATION:
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```
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
; AUTHORS: El Deiry et al.
; TITLE: "Human genomic DNA sequences define a
; consensus binding site for p53"
; JOURNAL: Nature Genetics
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
;
US-08-477-504A-21

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
Db 10 GGACTAGCT 2

RESULT 101
US-08-486-756A-21/c
; Sequence 21, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
; AUTHORS: El Deiry et al.
; TITLE: "Human genomic DNA sequences define a
; consensus binding site for p53"
; JOURNAL: Nature Genetics
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
;
US-08-485-862B-21

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
Db 10 GGACTAGCT 2

RESULT 102
US-08-485-862B-21/c
; Sequence 21, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
; AUTHORS: El Deiry et al.
; TITLE: "Human genomic DNA sequences define a
; consensus binding site for p53"
; JOURNAL: Nature Genetics
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
;
US-08-485-862B-21
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Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
||| |||
Db 10 GGACTAGCT 2

RESULT 103

US-08-388-353-703
; Sequence 703, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 703:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-703

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
||| |||
Db 2 CTCCTGGC 10

RESULT 104

US-08-388-353-704
; Sequence 704, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 704:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-704

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
||| |||
Db 1 CTCCTGGC 9

RESULT 105

US-08-388-353-769/c
; Sequence 769, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 769:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-770

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 10 GGCACACAC 2

RESULT 106
US-08-388-353-770/c
Sequence 770, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Leamont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 770:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-770

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 9 GGCACAC 1
RESULT 107
US-08-488-551B-703
Sequence 703, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 703:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-703

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGCG 14
Db 2 CTCCTGCG 10

RESULT 108
US-08-488-551B-704
Sequence 704, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

rn1

```

; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 704:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-704

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 6 CTCGCTGGC 14
Db 1 CTCCTGGC 9

```

```

RESULT 109
US-08-488-551B-769/c
; Sequence 769, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 769:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-769

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 12 GGCACGCAC 20
Db 10 GGCACACAC 2

```

```

RESULT 110
US-08-488-551B-770/c
; Sequence 770, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353

```

```

; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-770

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 12 GGCACGCAC 20
Db 9 GGCACGCAC 1

```

RESULT 111

```

US-08-793-398-1
; Sequence 1, Application US/08793398
; Patent No. 6030776
; GENERAL INFORMATION:
; TITLE OF INVENTION: Parallel SELEX
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,398
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WC PCT/US95/11982
; FILING DATE:
; APPLICATION NUMBER: US 08/309,245
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/714,131
; FILING DATE: 10-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/536,428
; FILING DATE: 11-JUN-1990
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-793-398-1

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 10 CTGGCAGC 18
Db 2 CAGGCACGC 10

```

RESULT 112

```

US-09-157-601-1
; Sequence 1, Application US/09157601
; Patent No. 6048698
; GENERAL INFORMATION:
; APPLICANT: EATON, BRUCE; GOLD, LARRY
; TITLE OF INVENTION: PARALLEL SELEX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,601
; FILING DATE: September 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,700
; FILING DATE: March 20, 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,245
; FILING DATE: 20-SEPTEMBER-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX22/CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-157-601-1

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 10 CTGGCAGC 18
Db 2 CAGGCACGC 10

```

RESULT 113

```

US-08-487-077A-21/c
; Sequence 21, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
; AUTHORS: El Deiry et al.
; TITLE: "Human genomic DNA sequences define a
; consensus binding site for p53"
; JOURNAL: Nature Genetics
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
; US-08-487-077A-21

```

```

Query Match          37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GGACTCGCT 11
    |||||
DB 10 GGACTAGCT 2

```

```

RESULT 114
US-08-485-863A-21/c
; Sequence 21, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:

```

```

; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
; AUTHORS: El Deiry et al.
; TITLE: "Human genomic DNA sequences define a
; consensus binding site for p53"
; JOURNAL: Nature Genetics
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
; US-08-485-863A-21

```

```

Query Match          37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GGACTCGCT 11
    |||||
DB 10 GGACTAGCT 2

```

```

RESULT 115

```

```

US-08-485-049D-21/c
; Sequence 21, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,049D
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-0332
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

```



```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
;   AUTHORS: El Deiry et al.
;   TITLE: "Human genomic DNA sequences define a
;   TITLE: consensus binding site for p53"
;   JOURNAL: Nature Genetics
;   VOLUME: 1
;   PAGES: 44-49
;   DATE: 1992
;   US-08-485-049D-21

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGACTGCT 11
Db 10 GGACTAGCT 2

RESULT 116
US-08-899-241-240/c
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huemelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; EARLIER FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
; US-08-899-241-240

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 10 ACGCGCTGG 2

RESULT 117
US-09-255-899-4
; Sequence 4, Application US/09255899
; Patent No. 6368663
; GENERAL INFORMATION:
; APPLICANT: Ecker et al.
; TITLE OF INVENTION: Reagents And Methods For Modulating Gene
; TITLE OF INVENTION: Expression Through RNA Mimicry
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6368663ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 MB

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: p53 binding site
; PUBLICATION INFORMATION:
;   AUTHORS: El Deiry et al.
;   TITLE: "Human genomic DNA sequences define a
;   TITLE: consensus binding site for p53"
;   JOURNAL: Nature Genetics
;   VOLUME: 1
;   PAGES: 44-49
;   DATE: 1992
;   US-08-485-049D-21

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGACTGCT 11
Db 10 GGACTAGCT 2

RESULT 116
US-08-899-241-240/c
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huemelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; EARLIER FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
; US-08-899-241-240

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 10 ACGCGCTGG 2

RESULT 117
US-09-255-899-4
; Sequence 4, Application US/09255899
; Patent No. 6368663
; GENERAL INFORMATION:
; APPLICANT: Ecker et al.
; TITLE OF INVENTION: Reagents And Methods For Modulating Gene
; TITLE OF INVENTION: Expression Through RNA Mimicry
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6368663ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 MB

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,899
; FILING DATE: 23-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1998
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-255-899-4

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14
Db 2 CUCUCUGGC 10

RESULT 118
US-09-989-789-567/c
; Sequence 567, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-989-789-567

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGCTGGCAC 16
Db 9 CGCTGGCAC 1

RESULT 119
US-09-989-789-568/c
; Sequence 568, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

```

;; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
;; FILE REFERENCE: 9325-0011.20 / S11-US2
;; CURRENT APPLICATION NUMBER: US/09/989,789
;; CURRENT FILING DATE: 2002-03-25
;; NUMBER OF SEQ ID NOS: 4085
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 568
;; TYPE: DNA
;; LENGTH: 10
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example target
;; OTHER INFORMATION: DNA
US-09-989-789-568

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGCCAC 16
Db 9 CGCTGCCAC 1

RESULT 120
PCT-US91-01822A-4
;; Sequence 4, Application PC/TUS9101822A
;; GENERAL INFORMATION:
;; APPLICANT: Ecker et al.
;; TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING
;; TITLE OF INVENTION: GENE EXPRESSION THROUGH RNA MIMICRY
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & Norris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/02628
;; FILING DATE: 19910417
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 497,090
;; FILING DATE: March 21, 1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jane Massey Licata
;; REGISTRATION NUMBER: 32,257
;; REFERENCE/DOCKET NUMBER: ISIS-0109
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
PCT-US91-01822A-4

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGCCAC 16
Db 9 CGCTGCCAC 1

RESULT 120
PCT-US91-01822A-4
;; Sequence 4, Application PC/TUS9101822A
;; GENERAL INFORMATION:
;; APPLICANT: Ecker et al.
;; TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING
;; TITLE OF INVENTION: GENE EXPRESSION THROUGH RNA MIMICRY
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & Norris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/01822A
;; FILING DATE: 19910319
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 497,090
;; FILING DATE: March 21, 1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jane Massey Licata
;; REGISTRATION NUMBER: 32,257
;; REFERENCE/DOCKET NUMBER: ISIS-0109
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
PCT-US91-01822A-4

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGCCAC 16
Db 9 CGCTGCCAC 1

Db 2 CUCUCUGGC 10

RESULT 121
PCT-US91-02628-4
;; Sequence 4, Application PC/TUS9102628
;; GENERAL INFORMATION:
;; APPLICANT: Ecker et al.
;; TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING
;; TITLE OF INVENTION: GENE EXPRESSION THROUGH RNA MIMICRY
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & Norris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/02628
;; FILING DATE: 19910417
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 497,090
;; FILING DATE: March 21, 1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jane Massey Licata
;; REGISTRATION NUMBER: 32,257
;; REFERENCE/DOCKET NUMBER: ISIS-0109
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
PCT-US91-02628-4

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 86.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
Db 2 CUCUCUGGC 10

RESULT 122
PCT-US95-11982-1
;; Sequence 1, Application PC/TUS9511982
;; GENERAL INFORMATION:
;; APPLICANT: EATON, BRUCE; GOLD, LARRY
;; TITLE OF INVENTION: PARALLEL SELEX
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson & Bratschun, L.L.C.
;; STREET: 8400 East Prentice Avenue, Suite
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS-DOS

QY 6 CTCGCTGGC 14
Db 2 CUCUCUGGC 10

; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,245
; FILING DATE: 20-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BARRY J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEW22/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-11982-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGCACGC 18
Db 2 CAGGCACGC 10
|||||

RESULT 123
PCT-US95-11982A-1
; Sequence 1, Application PC/TUS9511982A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Parallel SELEX
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11982A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,245
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/714,131
; FILING DATE: 10-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/536,428
; FILING DATE: 11-JUN-1990
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-11982A-1

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGCACGC 18
Db 2 CAGGCACGC 10
|||||

RESULT 124
US-09-249-155A-89
; Sequence 89 Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-249-155A-89

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 1 ACTGGCTGG 9
|||||

RESULT 125
US-09-249-155A-177/c
; Sequence 177 Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-249-155A-177

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
Db 11 ACTGGCTGG 3
|||||

RESULT 126

US-08-480-173A-18/c
 ; Sequence 18, Application US/08480173A
 ; Patent No. 6072049
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoma, Hans A
 ; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Popovich & Wiles, P.A.
 ; STREET: 80 S. 8th Street, Suite 1902
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,173A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Popovich, Thomas E
 ; REGISTRATION NUMBER: 30,099
 ; REFERENCE/DOCKET NUMBER: MED1003USD4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-334-8991
 ; TELEFAX: 612-334-8994
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (synthetic)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1..4
 ; OTHER INFORMATION: /note= "Nucleotides 1-4 form a
 ; OTHER INFORMATION: single-stranded "sticky end"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 5..8
 ; OTHER INFORMATION: /note= "Adapter sequence results
 ; OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 4-7 of
 ; OTHER INFORMATION: SEQ ID NO: 17"
 US-08-480-173A-18

Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGACTCG 9
 |||||
 Db 8 GGACTCG 2

RESULT 127

US-08-859-954-148
 ; Sequence 148, Application US/08859954
 ; Patent No. 6083695
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramin
 ; APPLICANT: Hardin, Paul E.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,954
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/632,782
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 148:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 US-08-859-954-148

Query Match 35.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACT 7
 |||||
 Db 2 ATGGACT 8

RESULT 128

US-08-484-408A-18/c
 ; Sequence 18, Application US/08484408A
 ; Patent No. 6117653
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoma, Hans A
 ; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Popovich & Wiles, P.A.
 ; STREET: 80 S. 8th Street, Suite 1902
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,408A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Popovich, Thomas E
 ; REGISTRATION NUMBER: 30,099

```
; REFERENCE/DOCKET NUMBER: MED1003USD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-334-8991
; TELEFAX: 612-334-8994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4_
; OTHER INFORMATION: /note= "Nucleotides 1-4 form a
; OTHER INFORMATION: single-stranded "sticky end"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5..8_
; OTHER INFORMATION: /note= "Adapter sequence results
; OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 4-7 of
; OTHER INFORMATION: SEQ ID NO: 17"
US-08-484-408A-18
```

```
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 GGACTCG 9
Db 8 GGACTCG 2
```

RESULT 129

```
US-09-398-499-1
; Sequence 1, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-1
```

```
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 CGCTGGC 14
Db 1 CGCTGGC 7
```

RESULT 130

```
US-09-398-499-6
; Sequence 6, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
```

```
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-6
```

```
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 CGCTGGC 14
Db 2 CGCTGGC 8
```

RESULT 131

```
US-09-398-499-24/c
; Sequence 24, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-24
```

```
Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 CGCTGGC 14
Db 8 CGCTGGC 2
```

RESULT 132

```
US-09-398-499-29/c
; Sequence 29, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-29
```

US-09-398-499-29

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGC 14
Db 7 CGCTGGC 1

RESULT 133

US-08-362-495-3/c
; Sequence 3, Application US/08362495
; Patent No. 6087171
; GENERAL INFORMATION:
; APPLICANT: Neuman, Toomas
; APPLICANT: Suda, Kikuo
; TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
; TITLE OF INVENTION: NEURONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,495
; FILING DATE: 18-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/14614
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/301,416
; FILING DATE: 08-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,522
; FILING DATE: 15-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 05800.0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-362-495-3

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
Db 9 TGGCAGC 3

RESULT 134

US-09-989-789-2378
; Sequence 2378, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2378
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2378

Query Match 35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGC 14
Db 3 CGCTGGC 9

RESULT 135

US-09-398-499-53/c
; Sequence 53, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 53
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-398-499-53

Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGC 14
Db 10 CGCTGGC 4

RESULT 136

US-09-154-750A-41
; Sequence 41, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A

; CURRENT FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/059,153
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/079817
 ; PRIOR FILING DATE: 1998-03-30
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 41
 ; TYPE: DNA
 ; LENGTH: 10
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-154-750A-41

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GACTCGC 10
 Db 1 GACTCGC 7

RESULT 137

US-09-475-947A-182/c
 ; Sequence 182, Application US/09475947A
 ; Patent No. 6472154
 ; GENERAL INFORMATION:
 ; APPLICANT: Garner, Harold R.
 ; APPLICANT: Wren, Jonathan D.
 ; APPLICANT: Minna, John D.
 ; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
 ; FILE REFERENCE: US00667
 ; CURRENT APPLICATION NUMBER: US/09/475,947A
 ; CURRENT FILING DATE: 1999-12-31
 ; NUMBER OF SEQ ID NOS: 346
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 182
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: human
 US-09-475-947A-182

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACGCAC 20
 Db 10 CACGCAC 4

RESULT 138

US-09-769-482-33/c
 ; Sequence 33, Application US/09769482
 ; Patent No. 6566130
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOUL, JUDD W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKESHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: POYNUCLEOTIDE ARRAY
 ; CURRENT APPLICATION NUMBER: US/09/769,482
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 33
 ; LENGTH: 10

; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Oligonucleotide
 US-09-769-482-33

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACGCAC 20
 Db 10 CACGCAC 4

RESULT 139

US-08-750-655-1
 ; Sequence 1, Application US/08750655
 ; Patent No. 5811092
 ; GENERAL INFORMATION:
 ; APPLICANT: PANCHAUD, Elisabeth
 ; TITLE OF INVENTION: NEW NAMATOPHAGE AGENT AGAINST NEMATODES
 ; TITLE OF INVENTION: OF THE MELOIDOGYNE GENUS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
 ; STREET: 1180 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/750,655
 ; FILING DATE: 16-DEC-1996
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meilman, Edward A.
 ; REGISTRATION NUMBER: 24,735
 ; REFERENCE/DOCKET NUMBER: P/2129-23
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 382-0700
 ; TELEFAX: (212) 382-0888
 ; TELEX: 236925
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 US-08-750-655-1

Query Match 34.0%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGACTCGC 10
 Db 1 ATGGACTCGC 10

RESULT 140

US-08-388-353-669
 ; Sequence 669, Application US/08388353
 ; Patent No. 6010895

GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 669:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-669

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTG 12
|||
Db 1 GGTCTCTCTG 10

RESULT 141
US-08-388-353-670
Sequence 670, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 670:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-670

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTG 13
|||
Db 1 GGTCTCTCTG 10

RESULT 142
US-08-388-353-771/c
Sequence 771, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 771:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE	DNA (genomic)	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
US-08-388-353-771	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
QY	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
DB	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
US-08-488-551B-670	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
QY	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
DB	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
US-08-488-551B-669	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
QY	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
DB	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
US-08-488-551B-669	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0
QY	10 CTGGCAGCA 19	Query Match	34.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
DB	10 CGGCACACA 1	Best Local Similarity	80.0%	Score 6.8	DB 1	Length 10	Best Local Similarity	80.0%	Pred. No. 73	Mismatches	0	Indels	2	Gaps	0
		Matches	8	Conservative	0	Mismatches	0	Indels	2	Gaps	0	Indels	2	Gaps	0

STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 771:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-771

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CTGGCAGCA 19
DB 10 CGGGCACAC 1

RESULT 146
US-08-757-024-864
Sequence 864, Application US/08757024
Patent No. 6025339
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 864:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-864

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGGCAC 16
DB 1 TCGCGGGCAC 10

RESULT 147
US-08-297-395-59
Sequence 59, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
TITLE OF INVENTION: EPITOPE OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-08-297-395-59

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGC 14
DB 1 ACTAGCGGC 10

RESULT 148
US-08-878-835A-6/c
Sequence 6, Application US/08878835A
Patent No. 6337071
GENERAL INFORMATION:
APPLICANT: William Mitchell Molyneux
TITLE OF INVENTION: Mosquito and/or Flea Control
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: D. Peter Hochberg Co., L.P.A.
STREET: The Baker Building - Sixth Floor 1940 East 6th Street
STATE: Ohio
COUNTRY: U.S.A.

```

;
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MByte storage
; COMPUTER: IBM Compatible w/ Pentium Processor
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,835A
; FILING DATE: June 19, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PO 0605
; FILING DATE: 21 June 1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; US-08-878-835A-6
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 10 CTGGCAGCGCA 19
; Db 10 CTGGCTCGAA 1
;
; RESULT 149
; US-09-508-753B-195
; Sequence 195, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 195
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-508-753B-195
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 GGACTCGCTG 12
; Db 1 GGATTCAGT 10
;
; RESULT 150
; US-09-508-753B-289/c
; Sequence 289, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 195
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-508-753B-195
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 GGACTCGCTG 12
; Db 1 GGATTCAGT 10
;
; RESULT 151
; US-09-508-753B-387/c
; Sequence 387, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 387
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-508-753B-387
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 GGACTCGCTG 12
; Db 10 GAAATCGCTG 1
;
; RESULT 152
; US-09-508-753B-389
; Sequence 389, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIXI

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; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIXI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 289
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-508-753B-289
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 GGACTCGCTG 12
; Db 10 GGATTCAGT 1
;
; RESULT 151
; US-09-508-753B-387/c
; Sequence 387, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 387
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-508-753B-387
;
; Query Match 34.0%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 73;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 GGACTCGCTG 12
; Db 10 GAAATCGCTG 1
;
; RESULT 152
; US-09-508-753B-389
; Sequence 389, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIXI

```

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 389
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-389

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGACTCGCTG 12
| | | | |
Db 1 GAAATCGCTG 10

RESULT 153
US-08-894-454-132
; Sequence 132, Application US/08894454
; Patent No. 6544784
; GENERAL INFORMATION:
; APPLICANT: VAN DEN VEN, W.J.M.
; APPLICANT: SCHOENMAKERS, H.P.P.M.
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Webb Law Firm
; STREET: 700 Koppers Building, 436 Seventh Avenue
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219-1618
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,454
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP/00716
; FILING DATE: 19-FEB-1996
; APPLICATION NUMBER: 95200390.3
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: 95201951.1
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Barbara E
; REGISTRATION NUMBER: 31,198
; REFERENCE/DOCKET NUMBER: 702-971100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 412-471-8815
; TELEFAX: 412-471-4094
; TELEX:
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-894-454-132

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGACTCGC 10
| | | | |
Db 1 ATGGAGTCTC 10

RESULT 154
US-09-769-482-49/c
; Sequence 49, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POLYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-49

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TCGCTGGCAC 16
| | | | |
Db 10 TCACTGGAAC 1

RESULT 155
US-09-989-789-1268
; Sequence 1268, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1268

Query Match 34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-202

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
DB 8 ATGGCTC 1

RESULT 159
US-08-859-954-210
; Sequence 210, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-210

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCT 11
DB 1 GACTCTCT 8

RESULT 161
US-08-859-954-213/c
; Sequence 213, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-212

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCT 11
DB 1 GACTCTCT 8

RESULT 161
US-08-859-954-213/c
; Sequence 213, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-212
```

GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-213

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGTC 8
|||||
Db 8 ATGGAGTC 1

RESULT 162
US-08-859-954-403
Sequence 403, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 403:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-403

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGTC 8
|||||
Db 1 ATGGAGAC 6

RESULT 163
US-09-398-499-8
Sequence 8, Application US/09398499
Patent No. 6284466
GENERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-8

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCTGGCAC 16
|||||
Db 1 GCTGGCGC 8

RESULT 164
US-09-398-499-16
Sequence 16, Application US/09398499

```
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-16

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CTGGCAGC 17
        |||||
Db       1 CTGGCGCG 8

RESULT 165
US-09-398-499-31/c
; Sequence 31, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-31

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GCTGGCAC 16
        |||||
Db       8 GCTGGCGC 1

RESULT 166
US-09-398-499-39/c
; Sequence 39, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 39
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-39

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CTGGCAGC 17
        |||||
Db       8 CTGGCGCG 1

RESULT 167
US-08-488-015B-9
; Sequence 9, Application US/08488015B
; Patent No. 5780272
; GENERAL INFORMATION:
; APPLICANT: Jarrell, Kevin A.
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
; TITLE OF INVENTION: AND REAGENTS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,015B
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HUV-008.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-488-015B-9

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATGGACTC 8
        |||||
Db       2 AAGGACTC 9

RESULT 168
US-08-717-526-61
; Sequence 61, Application US/08717526
; Patent No. 5786147
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOULT, DIDIER
```


;; TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
;; NUMBER OF SEQUENCES: 79
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OLIFF & BERRIDGE
;; STREET: 700 SOUTH WASHINGTON STREET
;; CITY: ALEXANDRIA
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/717,526
;; FILING DATE: 17-SEP-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BERRIDGE, WILLIAM P.
;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 38732
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6400
;; TELEFAX: 703-836-2787
;; INFORMATION FOR SEQ ID NO: 61:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-717-526-61

Query Match 32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0;

Qy 5 ACTCGCTG 12
Db 1 ACTCTCTG 8

RESULT 169
US-08-360-051A-46
;; Sequence 46, Application US/08360051A
;; Patent No. 5891681
;; GENERAL INFORMATION:
;; APPLICANT: Mallet, Francois
;; APPLICANT: Guillo-Bonnici, Francoise
;; APPLICANT: Cleuziat, Philippe
;; APPLICANT: Levasseur, Pierre
;; TITLE OF INVENTION: MODIFIED PROMOTER FOR RNA POLYMERASE,
;; TITLE OF INVENTION: ITS PREPARATION AND ITS APPLICATIONS
;; NUMBER OF SEQUENCES: 65
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OLIFF & BERRIDGE
;; STREET: 700 South Washington Street, Suite 300
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/360,051A
;; FILING DATE: 20-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Berridge, William P.

;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 36049
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6400
;; TELEFAX: 703-836-2787
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "DNA"
;; US-08-360-051A-46

Query Match 32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0;

Qy 4 GACTCGCT 11
Db 2 GACTCACT 9

RESULT 170
US-08-796-899-17/c
;; Sequence 17, Application US/08796899
;; Patent No. 6160202
;; GENERAL INFORMATION:
;; APPLICANT: BUSTOS, Mauricio M
;; APPLICANT: CHERN, Maw-Sheng
;; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
;; TITLE OF INVENTION: TRANSCRIPTION FACTORS
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/796,899
;; FILING DATE: 06-FEB-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/319,544
;; FILING DATE: 07-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 028754-005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-8620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-796-899-17

Query Match 32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0;


```
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-677-218B-48

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
Db 9 ATGGTCTC 2

RESULT 174
US-09-677-192-48/c
; Sequence 48, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-192-48

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
Db 9 ATGGTCTC 2

RESULT 175
US-09-380-836-4
; Sequence 4, Application US/09380836
; Patent No. 6551775
; GENERAL INFORMATION:
; APPLICANT: Lifton, Richard P.
; APPLICANT: Chang, Sue S.
; APPLICANT: Rossier, Bernard C.
; TITLE OF INVENTION: Method to Diagnose and Treat Pathological Conditions
; TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
; TITLE OF INVENTION: Pseudohypoadosteronism Type-1
; FILE REFERENCE: 44574-5018-US
```

```
; CURRENT APPLICATION NUMBER: US/09/380,836
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/040,171
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US98/04681
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Segment of mutant alpha ENaC allele
US-09-380-836-4

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGTCAGC 8

RESULT 176
US-09-989-789-2195/c
; Sequence 2195, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2195
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2195

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCGCT 11
Db 9 GACTCCCT 2

RESULT 177
US-09-958-221A-7
; Sequence 7, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 7
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-7

```

```

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      13 GCAGGCAC 20
Db      1 GCACACAC 8

```

```

RESULT 178
PCT-US96-01008-2
; Sequence 2, Application PC/TUS9601008
; GENERAL INFORMATION:
; APPLICANT: Hybridon, Inc.
; APPLICANT: Worcester Foundation for
; APPLICANT: Experimental Biology
; TITLE OF INVENTION: Human Immunodeficiency Virus
; TITLE OF INVENTION: Transcription Inhibitors and Methods of Their Use
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01008
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-037PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA or cDNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US96-01008-2

```

```

Query Match      32.0%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      6 CTCGCTGG 13
Db      1 CTCCTGG 8

```

```

Search completed: June 8, 2004, 12:28:07
Job time : 1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 12:25:33 ; Search time 0.001 Seconds
(without alignments)

187.440 Million cell updates/sec

Title: US-10-003-919-21

Perfect score: 20

Sequence: 1 ATGGACTCGTGGCAGCCAC 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 415 seqs, 4686 residues

Total number of hits satisfying chosen parameters: 830

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 415 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	Human Ship-1 antis
2	13.4	67.0	20	1	Primer for adenovi
3	13.4	67.0	20	1	Capture oligonucle
4	13.2	66.0	20	1	Human REQL2 antis
5	13	65.0	18	1	Human RECQL2 antis
6	12	60.0	16	1	TRADD antisense ol
7	11.8	59.0	18	1	NOT304 polymorphis
8	11.8	59.0	18	1	PCR primer #2 used
9	11.2	56.0	17	1	Human T125 CDNA am
10	11.2	56.0	17	1	Adaptor directed p
11	11.2	56.0	17	1	Human GMPLP-1 17-m
12	11	55.0	11	1	Mouse p21WAF1 CCG
13	10.4	52.0	12	1	NheI 5' PCR primer
14	10.4	52.0	12	1	Tag sequence of a
15	10.4	52.0	15	1	Human pancreatic c
16	10.4	52.0	16	1	Lambda vector base
17	10.2	51.0	15	1	Human blaIIc po
18	10.2	51.0	15	1	IGFBP2 oligonucleo
19	10.2	51.0	15	1	Human SLC6A4 allel
20	10.2	51.0	15	1	Anti-HCV nucleic a
21	10.2	51.0	15	1	Anti-HCV enzymatic
22	10	50.0	11	1	Human skin EST 911
23	10	50.0	11	1	Human skin EST 169
24	10	50.0	12	1	Sample preparation
25	10	50.0	12	1	Sample preparation
26	10	50.0	15	1	Human CERP HH ribo
27	10	50.0	15	1	M. avium 16S rRNA
28	9.8	49.0	15	1	Human CERP HH ribo
29	9.8	49.0	15	1	Primer NGFTE-4 use
30	9.8	49.0	15	1	Alpha2 integrin pr
31	9.8	49.0	15	1	Human fit-1 and KD
32	9.8	49.0	15	1	Human FKBP8 allel
33	9.8	49.0	15	1	IGFBP2 oligonucleo

34	9.8	49.0	15	1	AAF45240	IGFBP2 oligonucleo
35	9.8	49.0	15	1	AAF45957	IGFBP2 oligonucleo
36	9.8	49.0	15	1	AAF45236	IGFBP2 oligonucleo
37	9.8	49.0	15	1	AAF45242	IGFBP2 oligonucleo
38	9.8	49.0	15	1	AAF45237	IGFBP2 oligonucleo
39	9.8	49.0	15	1	AAF45241	IGFBP2 oligonucleo
40	9.8	49.0	15	1	AAF45956	IGFBP2 oligonucleo
41	9.8	49.0	15	1	ABL95817	Myeloid progenitor
42	9.8	49.0	15	1	ABT05310	Human N-acetylglala
43	9.8	49.0	15	1	ABT05310	RNA sequence #5, f
44	9.8	49.0	15	1	ABT05310	Left primer DDM011
45	9.4	47.0	11	1	ABV71404	Human skin EST 919
46	9.4	47.0	11	1	ABV63383	Human skin EST 176
47	9.4	47.0	12	1	AAV32268	Random primed reve
48	9.4	47.0	13	1	ABC22800	Oligonucleotide SE
49	9.4	47.0	13	1	ABC22801	Oligonucleotide SE
50	9.4	47.0	14	1	AAZ23798	HSV RNA fragment 1
51	9.2	46.0	14	1	ABV99924	Oligonucleotide SU
52	9.2	46.0	14	1	AD48184	Flu-2 PNA probe us
53	9.2	46.0	14	1	AD48185	Flu-3 PNA probe us
54	9.2	46.0	14	1	AD48186	Flu-4 PNA probe us
55	9	45.0	10	1	AAZ78944	Human dendritic ce
56	9	45.0	10	1	AAZ78405	Human dendritic ce
57	9	45.0	10	1	AAH64349	Human ubiquitously
58	9	45.0	10	1	AAZ45327	Human KCNB1 gene p
59	9	45.0	10	1	ABL52050	Human SC18A2 prof
60	9	45.0	11	1	ABV63868	Human skin EST 185
61	9	45.0	11	1	ABV71289	Human skin EST 907
62	9	45.0	11	1	ABV65042	Human skin EST 282
63	9	45.0	12	1	AAZ34403	Template sequence
64	9	45.0	12	1	AAZ34404	Kruppel system oli
65	9	45.0	13	1	AAZ92438	CFTR gene analysis
66	9	45.0	13	1	AAZ06013	Detection probe HD
67	9	45.0	13	1	AAZ40108	Detection probe HD
68	9	45.0	13	1	AAZ40248	Positive control 1
69	9	45.0	13	1	AAZ30135	Nucleotide sequenc
70	8.8	44.0	12	1	AAZ99838	Oligonucleotide pr
71	8.8	44.0	12	1	AB110648	Oligonucleotide pr
72	8.8	44.0	12	1	ABH86576	Oligonucleotide pr
73	8.8	44.0	12	1	ABH86514	Oligonucleotide pr
74	8.8	44.0	12	1	ABH86514	Oligonucleotide pr
75	8.8	44.0	12	1	ABH86495	Oligonucleotide pr
76	8.8	44.0	12	1	ABH86557	Oligonucleotide pr
77	8.8	44.0	12	1	AB110641	Oligonucleotide SE
78	8.8	44.0	13	1	ABC09578	Oligonucleotide SE
79	8.8	44.0	13	1	ABC09579	Oligonucleotide SE
80	8.8	44.0	13	1	ACD66039	Anti-HCV nucleic a
81	8.4	42.0	10	1	AAQ64030	16S rRNA gene frag
82	8.4	42.0	10	1	AAZ77589	Human dendritic ce
83	8.4	42.0	10	1	AAZ77589	Human dendritic ce
84	8.4	42.0	10	1	AAZ85891	Metastatic breast
85	8.4	42.0	10	1	AAZ83491	Metastatic breast
86	8.4	42.0	10	1	AAZ85754	Metastatic breast
87	8.4	42.0	10	1	AAZ6201	Human monocyte gen
88	8.4	42.0	10	1	AAZ79851	Human dendritic ce
89	8.4	42.0	10	1	AAH63566	Human ubiquitously
90	8.4	42.0	10	1	ABA06025	Human normal hepat
91	8.4	42.0	10	1	AAF41594	Yeast NORF gene SA
92	8.4	42.0	10	1	ABV84757	Chronic hepatitis
93	8.4	42.0	10	1	ABV84542	Human HCC underexp
94	8.4	42.0	10	1	ABV84505	Human apolipoprote
95	8.4	42.0	10	1	ABV84710	Human apolipoprote
96	8.4	42.0	10	1	ABV84791	Human apolipoprote
97	8.4	42.0	10	1	ABV84919	Human apolipoprote
98	8.4	42.0	10	1	ABN88036	Human SCYB14 prefe
99	8.4	42.0	10	1	ACA94471	DNA tag from human
100	8.4	42.0	10	1	ACA94472	DNA tag from human
101	8.4	42.0	11	1	AAQ85812	2'-O-alkylamino-co
102	8.4	42.0	11	1	ABQ86878	Human skin stress/
103	8.4	42.0	11	1	ABQ86878	Human skin stress/
104	8.4	42.0	11	1	ABQ87015	Human skin stress/
105	8.4	42.0	11	1	ABQ86921	Human skin stress/
106	8.4	42.0	11	1	ABQ87551	Human skin stress/

107	8.4	42.0	11	1	ABV63288	Human skin EST 107	C 180	8	40.0	11	1	ABV72049	Human skin EST 983
108	8.4	42.0	11	1	ABV71227	Human skin EST 901	C 181	8	40.0	11	1	ABV68016	Human skin EST 580
109	8.4	42.0	11	1	ABV70887	Human skin EST 867	C 182	8	40.0	11	1	ABV69750	Human skin EST 753
110	8.4	42.0	11	1	ABV63627	Human skin EST 141	C 183	8	40.0	11	1	ABV63949	Human skin EST 173
111	8.4	42.0	11	1	ABV63806	Human skin EST 159	C 184	8	40.0	11	1	ABV65067	Human skin EST 285
112	8.4	42.0	11	1	ABV71048	Human skin EST 883	C 185	8	40.0	11	1	ABV71370	Human skin EST 915
113	8.4	42.0	11	1	ABV70709	Human skin EST 849	C 186	8	40.0	11	1	ABV64955	Human skin EST 274
114	8.4	42.0	11	1	ABV63167	Human skin EST 953	C 187	8	40.0	11	1	ABV68998	Human skin EST 678
115	8.4	42.0	11	1	ABV68745	Human skin EST 653	C 188	8	40.0	11	1	ABV71590	Human skin EST 937
116	8.4	42.0	11	1	ABV69231	Human skin EST 701	C 189	8	40.0	11	1	ABK47234	Nucleic acid analy
117	8.4	42.0	11	1	ABV63466	Human skin EST 125	C 190	8	40.0	12	1	AAV54872	C/EBP-beta antisen
118	8.4	42.0	11	1	ABV70588	Human skin EST 837	C 191	8	40.0	12	1	AAV54405	Template sequence
119	8.4	42.0	11	1	ABV65542	Human skin EST 332	C 192	8	40.0	12	1	AAV54319	Human adenosine re
120	8.4	42.0	11	1	ABV65566	Human skin EST 335	C 193	8	40.0	12	1	AAV54044	Human C/EBP polyu
121	8.4	42.0	12	1	AAV50511	Sequence of one of	C 194	8	40.0	12	1	ABH86538	Oligonucleotide pr
122	8.4	42.0	12	1	AAV55521	Immunosuppressant	C 195	8	40.0	12	1	ABH86538	Oligonucleotide pr
123	8.4	42.0	12	1	ACC58710	Input molecule for	C 196	8	40.0	12	1	ABH86538	Oligonucleotide pr
124	8	40.0	8	1	AAV60866	A. thaliana primer	C 197	8	40.0	12	1	ABH86538	Oligonucleotide pr
125	8	40.0	9	1	AAV60738	Human immune gene	C 198	8	40.0	12	1	ABH86538	Oligonucleotide pr
126	8	40.0	10	1	AAV60791	Primer for product	C 199	8	40.0	12	1	ABH86538	Oligonucleotide pr
127	8	40.0	10	1	AAV60939	Syngeneic and allo	C 200	8	40.0	12	1	ABH86538	Oligonucleotide pr
128	8	40.0	10	1	AAV60816	Arbitrary 5' oligo	C 201	8	40.0	12	1	ABH86538	Oligonucleotide pr
129	8	40.0	10	1	AAV60816	Arbitrary RT-PCR p	C 202	8	40.0	12	1	ABH86538	Oligonucleotide pr
130	8	40.0	10	1	AAV60888	Human breast cancer	C 203	8	40.0	12	1	ABH86538	Oligonucleotide pr
131	8	40.0	10	1	AAV60888	Human breast cancer	C 204	8	40.0	12	1	ABH86538	Oligonucleotide pr
132	8	40.0	10	1	AAV60888	Human breast cancer	C 205	8	40.0	12	1	ABH86538	Oligonucleotide pr
133	8	40.0	10	1	AAV60888	Human breast cancer	C 206	8	40.0	12	1	ABH86538	Oligonucleotide pr
134	8	40.0	10	1	AAV60888	Human breast cancer	C 207	8	40.0	12	1	ABH86538	Oligonucleotide pr
135	8	40.0	10	1	AAV60888	Human breast cancer	C 208	8	40.0	12	1	ABH86538	Oligonucleotide pr
136	8	40.0	10	1	AAV60888	Human breast cancer	C 209	8	40.0	12	1	ABH86538	Oligonucleotide pr
137	8	40.0	10	1	AAV60888	Human breast cancer	C 210	8	40.0	12	1	ABH86538	Oligonucleotide pr
138	8	40.0	10	1	AAV60888	Human breast cancer	C 211	8	40.0	12	1	ABH86538	Oligonucleotide pr
139	8	40.0	10	1	AAV60888	Human breast cancer	C 212	8	40.0	12	1	ABH86538	Oligonucleotide pr
140	8	40.0	10	1	AAV60888	Human breast cancer	C 213	8	40.0	12	1	ABH86538	Oligonucleotide pr
141	8	40.0	10	1	AAV60888	Human breast cancer	C 214	8	40.0	12	1	ABH86538	Oligonucleotide pr
142	8	40.0	10	1	AAV60888	Human breast cancer	C 215	8	40.0	12	1	ABH86538	Oligonucleotide pr
143	8	40.0	10	1	AAV60888	Human breast cancer	C 216	8	40.0	12	1	ABH86538	Oligonucleotide pr
144	8	40.0	10	1	AAV60888	Human breast cancer	C 217	8	40.0	12	1	ABH86538	Oligonucleotide pr
145	8	40.0	10	1	AAV60888	Human breast cancer	C 218	8	40.0	12	1	ABH86538	Oligonucleotide pr
146	8	40.0	10	1	AAV60888	Human breast cancer	C 219	8	40.0	12	1	ABH86538	Oligonucleotide pr
147	8	40.0	10	1	AAV60888	Human breast cancer	C 220	8	40.0	12	1	ABH86538	Oligonucleotide pr
148	8	40.0	10	1	AAV60888	Human breast cancer	C 221	8	40.0	12	1	ABH86538	Oligonucleotide pr
149	8	40.0	10	1	AAV60888	Human breast cancer	C 222	8	40.0	12	1	ABH86538	Oligonucleotide pr
150	8	40.0	10	1	AAV60888	Human breast cancer	C 223	8	40.0	12	1	ABH86538	Oligonucleotide pr
151	8	40.0	10	1	AAV60888	Human breast cancer	C 224	8	40.0	12	1	ABH86538	Oligonucleotide pr
152	8	40.0	10	1	AAV60888	Human breast cancer	C 225	8	40.0	12	1	ABH86538	Oligonucleotide pr
153	8	40.0	10	1	AAV60888	Human breast cancer	C 226	8	40.0	12	1	ABH86538	Oligonucleotide pr
154	8	40.0	10	1	AAV60888	Human breast cancer	C 227	8	40.0	12	1	ABH86538	Oligonucleotide pr
155	8	40.0	10	1	AAV60888	Human breast cancer	C 228	8	40.0	12	1	ABH86538	Oligonucleotide pr
156	8	40.0	10	1	AAV60888	Human breast cancer	C 229	8	40.0	12	1	ABH86538	Oligonucleotide pr
157	8	40.0	10	1	AAV60888	Human breast cancer	C 230	8	40.0	12	1	ABH86538	Oligonucleotide pr
158	8	40.0	10	1	AAV60888	Human breast cancer	C 231	8	40.0	12	1	ABH86538	Oligonucleotide pr
159	8	40.0	10	1	AAV60888	Human breast cancer	C 232	8	40.0	12	1	ABH86538	Oligonucleotide pr
160	8	40.0	10	1	AAV60888	Human breast cancer	C 233	8	40.0	12	1	ABH86538	Oligonucleotide pr
161	8	40.0	10	1	AAV60888	Human breast cancer	C 234	8	40.0	12	1	ABH86538	Oligonucleotide pr
162	8	40.0	10	1	AAV60888	Human breast cancer	C 235	8	40.0	12	1	ABH86538	Oligonucleotide pr
163	8	40.0	10	1	AAV60888	Human breast cancer	C 236	8	40.0	12	1	ABH86538	Oligonucleotide pr
164	8	40.0	10	1	AAV60888	Human breast cancer	C 237	8	40.0	12	1	ABH86538	Oligonucleotide pr
165	8	40.0	10	1	AAV60888	Human breast cancer	C 238	8	40.0	12	1	ABH86538	Oligonucleotide pr
166	8	40.0	10	1	AAV60888	Human breast cancer	C 239	8	40.0	12	1	ABH86538	Oligonucleotide pr
167	8	40.0	10	1	AAV60888	Human breast cancer	C 240	8	40.0	12	1	ABH86538	Oligonucleotide pr
168	8	40.0	10	1	AAV60888	Human breast cancer	C 241	8	40.0	12	1	ABH86538	Oligonucleotide pr
169	8	40.0	10	1	AAV60888	Human breast cancer	C 242	8	40.0	12	1	ABH86538	Oligonucleotide pr
170	8	40.0	10	1	AAV60888	Human breast cancer	C 243	8	40.0	12	1	ABH86538	Oligonucleotide pr
171	8	40.0	10	1	AAV60888	Human breast cancer	C 244	8	40.0	12	1	ABH86538	Oligonucleotide pr
172	8	40.0	10	1	AAV60888	Human breast cancer	C 245	8	40.0	12	1	ABH86538	Oligonucleotide pr
173	8	40.0	10	1	AAV60888	Human breast cancer	C 246	8	40.0	12	1	ABH86538	Oligonucleotide pr
174	8	40.0	10	1	AAV60888	Human breast cancer	C 247	8	40.0	12	1	ABH86538	Oligonucleotide pr
175	8	40.0	10	1	AAV60888	Human breast cancer	C 248	8	40.0	12	1	ABH86538	Oligonucleotide pr
176	8	40.0	10	1	AAV60888	Human breast cancer	C 249	8	40.0	12	1	ABH86538	Oligonucleotide pr
177	8	40.0	10	1	AAV60888	Human breast cancer	C 250	8	40.0	12	1	ABH86538	Oligonucleotide pr
178	8	40.0	10	1	AAV60888	Human breast cancer	C 251	8	40.0	12	1	ABH86538	Oligonucleotide pr
179	8	40.0	10	1	AAV60888	Human breast cancer	C 252	8	40.0	12	1	ABH86538	Oligonucleotide pr

253	7.8	39.0	12	1	AAH79164	Oligonucleotide OD
254	7.8	39.0	12	1	AAH79164	Microarray capture
255	7.8	39.0	12	1	AAF56190	Microarray capture
256	7.8	39.0	12	1	AAH56187	Synthetic k-ras co
257	7.8	39.0	12	1	AAH65968	Synthetic k-ras co
258	7.8	39.0	12	1	AAH65971	Oligonucleotide pr
259	7.8	39.0	12	1	AAH83492	Oligonucleotide pr
260	7.8	39.0	12	1	AAH91416	Oligonucleotide pr
261	7.8	39.0	12	1	AAH10618	Oligonucleotide pr
262	7.8	39.0	12	1	AAH85734	Oligonucleotide pr
263	7.8	39.0	12	1	AAH86519	Oligonucleotide pr
264	7.8	39.0	12	1	AAH90187	Oligonucleotide pr
265	7.8	39.0	12	1	AAH94001	Oligonucleotide pr
266	7.8	39.0	12	1	AAH12556	Oligonucleotide pr
267	7.8	39.0	12	1	AAH178918	Oligonucleotide pr
268	7.8	39.0	12	1	AAH74993	Oligonucleotide pr
269	7.8	39.0	12	1	AAH86581	Oligonucleotide pr
270	7.8	39.0	12	1	AAH802759	Human pregnane x r
271	7.8	39.0	12	1	AAH171695	AAV containing gro
272	7.8	39.0	12	1	AAH191654	SpeI 5' PCR primer
273	7.8	39.0	12	1	AAH45523	RC15 linker DNA us
274	7.8	39.0	12	1	AAH45522	RC14 linker DNA us
275	7.4	37.0	9	1	AAH91643	INVADER-directed c
276	7.4	37.0	9	1	AAH91989	Breast-cancer asso
277	7.4	37.0	9	1	AAH71918	Zinc finger protei
278	7.4	37.0	9	1	AAH71988	Zinc finger protei
279	7.4	37.0	9	1	AAH64315	Zinc finger target
280	7.4	37.0	9	1	AAH64316	Zinc finger target
281	7.4	37.0	9	1	AAH64245	Zinc finger target
282	7.4	37.0	10	1	AAH907131	HIV-1 NL4-3 LTR nu
283	7.4	37.0	10	1	AAH971136	HIV-1 NL4-3 LTR nu
284	7.4	37.0	10	1	AAH971137	HIV-1 NL4-3 LTR nu
285	7.4	37.0	10	1	AAH971070	HIV-1 NL4-3 LTR nu
286	7.4	37.0	10	1	AAH28375	DNA-PG-maleimide
287	7.4	37.0	10	1	AAH20692	TAR mimetic oligon
288	7.4	37.0	10	1	AAH01788	10mer oligonucleot
289	7.4	37.0	10	1	AAH03660	HIV-1 TAR mimetic
290	7.4	37.0	10	1	AAH278047	Human dendritic ce
291	7.4	37.0	10	1	AAH278118	Human dendritic ce
292	7.4	37.0	10	1	AAH278051	Human dendritic ce
293	7.4	37.0	10	1	AAH278139	Human dendritic ce
294	7.4	37.0	10	1	AAH278796	Human dendritic ce
295	7.4	37.0	10	1	AAH277705	Human dendritic ce
296	7.4	37.0	10	1	AAH285223	Metastatic breast
297	7.4	37.0	10	1	AAH281248	Metastatic breast
298	7.4	37.0	10	1	AAH280271	Metastatic breast
299	7.4	37.0	10	1	AAH280823	Metastatic breast
300	7.4	37.0	10	1	AAH283828	Metastatic breast
301	7.4	37.0	10	1	AAH284731	Metastatic breast
302	7.4	37.0	10	1	AAH284972	Metastatic breast
303	7.4	37.0	10	1	AAH285114	Metastatic breast
304	7.4	37.0	10	1	AAH286280	Metastatic breast
305	7.4	37.0	10	1	AAH286519	Metastatic breast
306	7.4	37.0	10	1	AAH284821	Metastatic breast
307	7.4	37.0	10	1	AAH28384	Metastatic breast
308	7.4	37.0	10	1	AAH286285	Metastatic breast
309	7.4	37.0	10	1	AAH285204	Metastatic breast
310	7.4	37.0	10	1	AAH284046	Metastatic breast
311	7.4	37.0	10	1	AAH281436	Metastatic breast
312	7.4	37.0	10	1	AAH286559	Metastatic breast
313	7.4	37.0	10	1	AAH281131	Metastatic breast
314	7.4	37.0	10	1	AAH28254	Metastatic breast
315	7.4	37.0	10	1	AAH58564	Human macrophage 9
316	7.4	37.0	10	1	AAH13669	DNA-PG conjugatio
317	7.4	37.0	10	1	AAH73637	Probe #7 for seque
318	7.4	37.0	10	1	AAH21642	Myelin basic prote
319	7.4	37.0	10	1	AAH167389	Human FKBP8 gene p
320	7.4	37.0	10	1	AAH167391	Human FKBP8 gene p
321	7.4	37.0	10	1	AAH167386	Human FKBP8 gene p
322	7.4	37.0	10	1	AAH65517	Human ubiquitously
323	7.4	37.0	10	1	AAH63853	Human ubiquitously
324	7.4	37.0	10	1	AAH64386	Human ubiquitously
325	7.4	37.0	10	1	AAH64387	Human ubiquitously
1	7.4	37.0	10	1	AAH64528	Human ubiquitously
2	7.4	37.0	10	1	AAH63816	Human ubiquitously
3	7.4	37.0	10	1	AAH64282	Human ubiquitously
4	7.4	37.0	10	1	AAH63370	Linker used to mak
5	7.4	37.0	10	1	AAH70422	Human DRD2 polymor
6	7.4	37.0	10	1	AAH83149	Ceruloplasmin (fer
7	7.4	37.0	10	1	AAH41238	Yeast NORF gene SA
8	7.4	37.0	10	1	AAH42074	Yeast NORF gene SA
9	7.4	37.0	10	1	AAH35970	Yeast NORF gene SA
10	7.4	37.0	10	1	AAH37397	Yeast NORF gene SA
11	7.4	37.0	10	1	AAH40204	Yeast NORF gene SA
12	7.4	37.0	10	1	AAH41236	Yeast NORF gene SA
13	7.4	37.0	10	1	AAH43023	Yeast NORF gene SA
14	7.4	37.0	10	1	AAH40185	Yeast NORF gene SA
15	7.4	37.0	10	1	AAH43779	Yeast NORF gene SA
16	7.4	37.0	10	1	AAH35822	Yeast NORF gene SA
17	7.4	37.0	10	1	AAH41117	Yeast NORF gene SA
18	7.4	37.0	10	1	AAH39261	Yeast NORF gene SA
19	7.4	37.0	10	1	AAH36425	Yeast NORF gene SA
20	7.4	37.0	10	1	AAH43192	Yeast NORF gene SA
21	7.4	37.0	10	1	AAH43700	Yeast NORF gene SA
22	7.4	37.0	10	1	AAH41118	Yeast NORF gene SA
23	7.4	37.0	10	1	AAH43100	Yeast NORF gene SA
24	7.4	37.0	10	1	AAH43372	Yeast NORF gene SA
25	7.4	37.0	10	1	AAH40677	Yeast NORF gene SA
26	7.4	37.0	10	1	AAH39321	Yeast NORF gene SA
27	7.4	37.0	10	1	AAH18719	Primer-extension o
28	7.4	37.0	10	1	AAH18723	Primer-extension o
29	7.4	37.0	10	1	AAH45325	Human KCMB1 gene p
30	7.4	37.0	10	1	AAH18285	Primer-extension o
31	7.4	37.0	10	1	AAH59299	Human F12 gene all
32	7.4	37.0	10	1	ABK93938	Human protein kina
33	7.4	37.0	10	1	ABK93921	Human protein kina
34	7.4	37.0	10	1	ABK93949	Human protein kina
35	7.4	37.0	10	1	ABK17006	Pyridoxal (Pyridox
36	7.4	37.0	10	1	AAH48062	Human CSF3 gene al
37	7.4	37.0	10	1	ABQ71448	Zinc finger protei
38	7.4	37.0	10	1	ABQ71449	Zinc finger protei
39	7.4	37.0	10	1	ABL57847	Hepatitis C virus
40	7.4	37.0	10	1	ABV78428	Human Th1 cell pre
41	7.4	37.0	10	1	ABV78506	Human Th1 cell pre
42	7.4	37.0	10	1	ABV84790	Chronic hepatitis
43	7.4	37.0	10	1	ABV84695	Chronic hepatitis
44	7.4	37.0	10	1	ABV84296	Human multiple chr
45	7.4	37.0	10	1	ABV84523	Human HCC underexp
46	7.4	37.0	10	1	ABV84764	Chronic hepatitis
47	7.4	37.0	10	1	ABV84972	Human ceruloplasmi
48	7.4	37.0	10	1	ABV84741	Chronic hepatitis
49	7.4	37.0	10	1	ABV84604	Human multiple HCC
50	7.4	37.0	10	1	AAH18891	Oligonucleotide #7
51	7.4	37.0	10	1	AAH59580	Human CALM1 gene a
52	7.4	37.0	10	1	AAH39813	SMOH polymorphism
53	7.4	37.0	10	1	ACA94531	DNA tag from human
54	7.4	37.0	10	1	ACA94571	DNA tag from human
55	7.4	37.0	10	1	ACA94570	DNA tag from human
56	7.4	37.0	10	1	ADA62596	Zinc finger target
57	7.4	37.0	10	1	ADA62597	Zinc finger target
58	7.4	37.0	10	1	ADD71772	Monoclonal related
59	7.4	37.0	10	1	ADD71264	Mouse Et gene 3' s
60	7.4	37.0	11	1	AAZ18867	Murine MRL SAGE ta
61	7.4	37.0	11	1	AAZ18779	Murine CS7BL/6 SAG
62	7.4	37.0	11	1	ABQ87660	Human skin stress/
63	7.4	37.0	11	1	ABQ87184	Human skin stress/
64	7.4	37.0	11	1	ABQ86321	Human skin stress/
65	7.4	37.0	11	1	ABQ87581	Human skin stress/
66	7.4	37.0	11	1	ABV64284	Human skin Est 207
67	7.4	37.0	11	1	ABV68538	Human skin Est 632
68	7.4	37.0	11	1	ABV70252	Human skin Est 803
69	7.4	37.0	11	1	ABV69501	Human skin Est 728
70	7.4	37.0	11	1	ABV66405	Human skin Est 419
71	7.4	37.0	11	1	ABV70632	Human skin Est 841
72	7.4	37.0	11	1	ABV71705	Human skin Est 949
73	7.4	37.0	11	1	ABV65118	Human skin Est 290

CC cancer cells far more efficiently than bone marrow cells
XX
SQ Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAGCA 19
| | | | |
Db 18 ACTCGCTGGCACTCA 4

RESULT 3
ABI92928/c
ID ABI92928 standard; DNA; 20 BP.

XX AC ABI92928;

XX DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#15 oligo #9.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN W0200179548-A2.

XX XX 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX XX (CORR) CORNELL RES FOUND INC.

XX PA Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX PI WPI; 2002-034366/04.

XX DR Designing capture oligonucleotide probes for use on a support to which

XX PT complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 29; 300pp; English.

XX CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI92074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification

CC of the present invention
XX
SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGCAC 20
| | | | |
Db 19 CTGGCTGGCAGCAC 5

RESULT 4
AAD41745/c
ID AAD41745 standard; DNA; 20 BP.

XX AC AAD41745;

XX DT 30-OCT-2002 (first entry)

XX DE Human RECQL2 antisense oligonucleotide, ISIS #137525.

XX KW Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;
KW inflammation; therapy; human; phosphorothioate; ss.
XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..20

FT FT /*tag= a

FT FT /mod_base= OTHER

FT FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT FT /*tag= b

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl nucleotides"

FT modified_base 3

FT FT /*tag= d

FT FT /mod_base= m5c

FT modified_base 7..8

FT FT /*tag= e

FT FT /mod_base= m5c

FT modified_base 11

FT FT /*tag= f

FT FT /mod_base= m5c

FT modified_base 15..17

FT FT /*tag= g

FT FT /mod_base= m5c

FT modified_base 16..20

FT FT /*tag= c

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl nucleotides"

FT modified_base 20

FT FT /*tag= h

FT FT /mod_base= m5c

XX US6399378-B1.

XX 04-JUN-2002.

XX 01-MAR-2001; 2001US-00798096.

XX 01-MAR-2001; 2001US-00798096.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Watt AT;

XX WPI; 2002-535979/57.

XX Antisense compounds targeted to nucleic acids encoding RECQL2 associated

PT with Bloom's disorder, for modulating RECQL2 expression and treating
 PT diseases e.g. tumors associated with expression of the RECQL2 in humans.
 PS Example 15; Col 44; 86pp; English.
 CC The invention relates to antisense compounds targetted to nucleic acid
 CC encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the
 CC expression of RECQL2. Antisense compounds of the invention are useful for
 CC treating diseases associated with expression of RECQL2, in humans. They
 CC are useful for diagnostics, therapeutics and as research reagent, e.g.
 CC prophylactically to prevent or delay infection, inflammation or tumour
 CC formation. They are also useful in antisense therapy. The present
 CC sequence is an antisense oligonucleotide targetted to human RECQL2 DNA
 CC
 XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 66.0%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 TGGACTCGCTGGCAGCA 19
 Db 18 TGGCTTGATGGCAGCA 1
 RESULT 5
 ID AA293489/c
 XX AA293489 standard; DNA; 18 BP.
 AC AA293489;
 XX
 XX 24-JUL-2000 (first entry)
 DT
 DE TRADD antisense oligonucleotide.
 KW
 KW TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
 KW programmed cell death; antisense; inhibition; treatment; therapy;
 KW septic shock; inflammation; cancer; antiinflammatory; human; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_binding complement(1..18)
 FT /tag= a
 FT /note= "Complementary to bases 811-794 of the human TRADD
 FT sequence described in GENESEQ record AA293431"
 PN
 XX WO200012527-A1.
 XX
 XX 09-MAR-2000.
 PD
 XX 25-AUG-1999; 99WO-US019614.
 XX
 XX 28-AUG-1998; 98US-00143212.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Cowseert LM;
 PI
 XX WPI; 2000-237846/20.
 DR
 XX
 XX New antisense compounds that limit the expression of human TRADD protein,
 PT useful in the treatment and diagnosis of cancer, inflammation and septic
 PT shock.
 PT
 XX Claim 3; Page 52; 85pp; English.
 PS
 CC The intracellular protein TRADD has been identified as a critical link
 CC between tumour necrosis factor (TNF) receptor binding and downstream
 CC activation of NF-kappa-B. Overexpression of native TRADD activates NF-
 CC kappa-B in the absence of TNF and dominant negative mutants of TRADD
 CC block TNF-induced NF-kappa-B activation. A second effect of TNF in many
 CC cell types is the induction of apoptosis (programmed cell death). TRADD

CC overexpression has been shown to mimic TNF induction of apoptosis as
 CC well. Data indicates that TRADD and other downstream effector proteins
 CC are the rate limiting step of TNF action and would therefore serve as the
 CC most efficient targets for inhibition of TNF-induced events. Antisense
 CC oligonucleotides capable of inhibiting TRADD function may therefore be
 CC useful in a number of therapeutic, diagnostic and research applications.
 CC Inhibiting expression of TRADD by contacting human cells or tissues with
 CC the antisense compound may be used to treat a disease or condition
 CC associated with TRADD expression, for example, septic shock, or
 CC inflammation, or cancer. TRADD antisense oligonucleotides of varying
 CC inhibitory capabilities are listed in GENESEQ records AA293438-293517.
 CC The antisense oligonucleotides exhibit enhanced inhibitory capabilities
 CC when they have 2'-MOE wings and a deoxy gap
 XX
 XX Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 65.0%; Score 13; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGACTCGCTGGC 14
 Db 18 TGGACTCGCTGGC 6
 RESULT 6
 ID ADC98469
 XX ADC98469 standard; DNA; 16 BP.
 AC ADC98469;
 XX
 XX 01-JAN-2004 (first entry)
 DT
 DE NOT304 polymorphism marker PCR primer B primer seq.
 KW
 KW low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
 KW single nucleotide polymorphism; SNP; PCR primer; ss; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003054218-A2.
 XX
 XX 03-JUL-2003.
 PD
 XX 19-DEC-2002; 2002WO-US040948.
 PF
 XX 20-DEC-2001; 2001US-0342711P.
 PR
 XX 04-NOV-2002; 2002US-0423559P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Jones KA, Valdes A, Townley DJ, Mangion J, Galwey N, Bennett S;
 PI McKay I, Schafer A;
 PI
 XX WPI; 2003-559156/52.
 DR
 XX
 XX Determining whether an individual is predisposed to susceptibility to low
 FT bone mineral density (BMD) and/or bone damage, involves identifying
 FT polymorphisms in associated genes.
 FT
 XX Example 8; Page 238; 246pp; English.
 PS
 XX The present invention describes a method of determining whether an
 CC individual is predisposed to susceptibility to low bone mineral density
 CC (BMD) and/or bone damage comprising identifying whether the individual
 CC has at least one polymorphism in a polynucleotide encoding a protein,
 CC where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
 CC see ADC98235 to ADC98315). An agent identified in an method from the
 CC present invention which can be used for the prevention or treatment of a
 CC disease resulting in susceptibility to low BMD and/or bone damage is
 CC useful in the manufacture of a medicament for use in modulating the
 CC susceptibility to low BMD and/or bone damage. The disease associated with

CC low BMD and/or bone damage is osteoporosis. The present PCR primer
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 16 BP; 2 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGACTCGCTGG 13
 |||||
 Db 1 TGGACTCGCTGG 12

RESULT 7

AAD33544/c

ID AAD33544 standard; DNA; 18 BP.

XX AC AAD33544;

XX DT 01-JUL-2002 (first entry)

XX PCR primer #2 used to analyse the distribution of human T125 mRNA.
 XX Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;
 KW neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
 KW heart disorder; ischaemic heart disease; neuroprotective; vulnery;

KW cardiovascular disorder; ischaemic heart disease; immunosuppressive;
 KW glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;
 KW fecal spleen; prostate disorder; inflammatory disease; Crohn's disease;
 KW proliferative disorder; gynaecological; haemostatic; antibacterial;
 KW systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic;
 KW cystostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser;
 KW hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer;
 KW apoptotic disorder; rheumatoid arthritis; cardiant; renal disorder;
 KW hepatotropic; antipeptidic; antiallergic; dermatological; virucide; PCR;
 KW primer; ss.

XX OS Homo sapiens.

XX PN US2002028508-A1.

XX PD 07-MAR-2002.

XX PF 21-FEB-2001; 2001US-00790264.

XX PR 23-APR-1998; 98US-00063363.

XX PR 22-JUN-1998; 98US-00065661.

XX PR 29-JUL-1998; 98US-00102705.

XX PR 23-APR-1999; 99US-00124538.

XX PR 22-JUN-1999; 99US-00298531.

XX PR 29-JUL-1999; 99US-00337930.

XX PA (HOLT/) HOLTZMAN D A.

XX PA (GOOD/) GOODEARL A D J.

XX PA (MCCA/) MCCARTHY S A.

XX PI Holtzman DA, Goodearl AD, McCarthy SA;

XX DR WPI; 2002-303420/34.

PT Novel TANGO polypeptides and nucleic acid molecules useful as modulating
 PT agents in regulating cellular processes and for diagnosing and treating
 PT heart, liver, lung, kidney, inflammatory and cellular proliferative
 PT disorders.

XX Example 6; Page 42; 138pp; English.

XX The invention relates to nucleic acids encoding a variety of proteins
 CC human T125 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175
 CC (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive,
 CC therapeutic and other uses. Polypeptide of the invention has the ability

CC to inhibit a proteinase activity, to modulate cell-cell interactions,
 CC haematopoiesis and the ability to modulate clotting. Polypeptide and
 CC polynucleotide of the invention are useful for diagnosing and treating
 CC disorder characterised by their aberrant expression or activity. The
 CC antibodies are useful as modulating agents in regulating a variety of
 CC cellular processes e.g. cell proliferation and/or cell differentiation.
 CC TANGO-139 is useful for treating kidney defects such as kidney failure,
 CC TANGO-125 is useful in wound healing and for treating cancer. TANGO-110
 CC is useful for treating neoplasia, TANGO-177 or WDNM-2 is useful for
 CC treating cancer, are useful to treat pancreatic disorders, such as
 CC pancreatitis, cerebrovascular disease, and tumours, and injury or trauma
 CC to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g.,
 CC ischaemic heart disease, cardiovascular disorders, such as ischaemic
 CC heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat
 CC renal (kidney) disorders, such as glomerular disease (e.g., acute and
 CC chronic glomerulonephritis), TANGO-175 is useful to treat uterine
 CC disorders, hyperplasia of the endometrium. TANGO-110 is useful to treat
 CC spleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-
 CC 125 treats prostate disorders, such as inflammatory diseases, Crohn's
 CC disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for
 CC treating proliferative disorders, inflammatory disorders. TANGO-175, or
 CC WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus, immune
 CC related disorders, e.g., immunodeficiency disorders, viral disorders,
 CC cell growth disorders, e.g., cancers and inflammatory disorders and
 CC apoptotic disorders. The nucleic acids of the invention are used in gene
 CC therapy. The present sequence is a PCR primer used to analyse the
 CC distribution of T125 mRNA in human tissues

XX Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 24;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGCTCGCTGGCAC 16
 |||||
 Db 17 TGGCTCGCAGGCAC 3

RESULT 8

AAD61442/c

ID AAD61442 standard; DNA; 18 BP.

XX AC AAD61442;

XX DT 15-JAN-2004 (first entry)

XX DE Human T125 cDNA amplifying PCR primer #2.

XX Human; TANGO; kidney failure; hyperplasia; inflammatory disorder; cancer;
 KW angiogenesis; haematopoietic disorder; pancreatic disorder; hyperextension;
 KW heart disorder; hepatic disorder; diabetes mellitus; placental disorder;
 KW cerebrovascular disease; Goodpasture's syndrome; cardiovascular disorder;
 KW foetal spleen associated disease; reproductive disorder; atherosclerosis;
 KW glomerular disease; intestinal disorder; proliferative disorder; tumour;
 KW ovulation disorder; testicular disorder; lung disorder; Crohn's disease;
 KW prostate disorder; Whipple's disease; haemophilia; anaemia; thalassaemia;
 KW gene therapy; tranquillizer; vulnery; vasotropic; psoriasis; leukaemia;
 KW jaundice; immunosuppressive; abortion; ischaemia; arthritis; allergy;
 KW asthma; PCR; primer; ss.

XX OS Homo sapiens.

XX PN US2003104447-A1.

XX PD 05-JUN-2003.

XX PF 11-OCT-2002; 2002US-00269353.

XX PR 23-APR-1998; 98US-00065661.

XX PR 23-APR-1999; 99US-00298531.

XX PR 21-FEB-2001; 2001US-00790264.

XX OS Homo sapiens.
 XX PN WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX DR WPI; 2002-179446/23.
 XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX PS Disclosure; SEQ ID NO 9915; 214pp; English.
 XX CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 56.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGGACTCGGTGGAC 16
 Db 16 AGGAGCTCGCAGGAAC 1
 RESULT 11
 ABNO9922/c

ID XX ABNO9922 standard; DNA; 17 BP.
 AC XX ABNO9922;
 DT XX 29-MAY-2002 (first entry)
 DE XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9914.
 KW XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW XX skeletal muscle disorder; amplicon; screening; ss.
 OS XX Homo sapiens.
 PN XX WO200192524-A2.
 PD XX 06-DEC-2001.
 PF XX 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX DR WPI; 2002-179446/23.
 XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX PS Disclosure; SEQ ID NO 9914; 214pp; English.
 XX CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 56.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGGCAC 16
 17 AGGACTCGCAGGAC 2

Db
 ABL91653/c
 ID ABL91653 standard; DNA; 11 BP.
 XX AAD27555;
 AC AAD27555;
 XX 18-APR-2002 (first entry)
 DT Mouse p21WAF1 CCGGG motif 5' flanking DNA.
 DE p53 protein; pGL3 luciferase reporter vector; luc+; transcription factor;
 KW cell cycle control; DNA damage repair; apoptosis; mouse; p21WAF1 DNA; ds.
 XX Mus sp.
 OS WO200196602-A2.
 PN 20-DEC-2001.
 XX 18-JUN-2001; 2001WO-GB002718.
 XX 16-JUN-2000; 2000GB-00014820.
 XX (MEDI-) MEDICAL RES COUNCIL.
 PA Yang AL, Festing M;
 PI WPI; 2002-130743/17.
 XX Determining the p53 status of a sample, useful for assaying for mimetics
 PT or antagonists of p53, or for the presence of DNA damage, comprises
 PT determining whether p53 binds to the pGL3 vector in a sample containing a
 PT pGL3 vector.
 XX Disclosure; Page 12; 53pp; English.

CC The patent discloses methods for determining the p53 status of a sample
 CC which comprise providing a sample containing a pGL3 luciferase reporter
 CC vector and determining whether p53 binds to the pGL3 vector. p53 is a
 CC transcription factor that regulates many genes including those associated
 CC with cell cycle control, apoptosis and DNA damage repair. pGL3 reporter
 CC vectors contain a modified firefly luciferase cDNA designated luc+. p53
 CC protein binds to pGL3-basic vector and causes luciferase expression. The
 CC method is useful for determining the p53 status of a sample. It is also
 CC useful for assaying for mimetics or antagonists of p53 and for assaying
 CC for presence of activated p53 and/or DNA damage. The invention also
 CC relates to a method of modifying pGL3 vector which involves deletion or
 CC alteration of a CCGGG motif of the pGL3 vector and/or deleting or
 CC altering a sequence within 20 bp sequence 5' or 3' of CCGGG motif. The
 CC nucleic acid having a sequence incorporating the CCGGG motif is useful
 CC for conferring promoter activity or p53-responsiveness on a nucleic acid
 CC encoding a polypeptide of interest or in assays for p53 transcriptional
 CC activity. The present DNA sequence is mouse p21WAF1 CCGGG motif 5'
 CC flanking DNA. This sequence is used along with CCGGG motif to confer
 CC promoter activity

XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 SQ Query Match 55.0%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
 |||||

Db 11 GACTCGCTGGC 1

RESULT 13
 ABL91653/c
 ID ABL91653 standard; DNA; 12 BP.
 XX ABL91653;
 AC ABL91653;
 XX 29-JUL-2002 (first entry)
 DT NheI 5' PCR primer tail used in Chlamydia pneumoniae gene amplification.
 XX Chlamydia pneumoniae; chlamydial infection; antigen; immunogen; vaccine;
 KW diagnosis; human respiratory disease; cardiovascular disease;
 KW atherosclerosis; coronary artery disease; carotid artery stenosis;
 KW myocardial infarction; cerebrovascular disease; aortic aneurysm;
 KW claudication; stroke; strain CWL029; open reading frame; ORF;
 KW Escherichia coli; recombinant expression; primer tail sequence; PCR;
 KW primer; ss.
 XX Synthetic.
 OS WO200202606-A2.
 PN 10-JAN-2002.
 XX 03-JUL-2001; 2001WO-IB001445.
 XX 03-JUL-2000; 2000GB-00016363.
 PR 11-JUL-2000; 2000GB-00017047.
 PR 21-JUL-2000; 2000GB-00017983.
 PR 07-AUG-2000; 2000GB-00019368.
 PR 18-AUG-2000; 2000GB-00020440.
 PR 14-SEP-2000; 2000GB-00022583.
 PR 10-NOV-2000; 2000GB-00027549.
 PR 22-DEC-2000; 2000GB-00031706.
 XX (CHIR-) CHIRON SPA.
 PA Ratti G, Grandi G;
 PI WPI; 2002-154726/20.
 DR Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
 XX Example; Page 33; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL9184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. Sequences ABL91352-ABL91657 represent PCR
 CC primer tail sequences containing restriction enzyme sites used in the
 CC exemplifications in the amplification of the novel Chlamydia pneumoniae
 CC open reading frames (ORFs) for cloning into Escherichia coli expression
 CC vectors

XX Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 52.0%; Score 10.4; DB 1; Length 12;

Best Local Similarity 91.7%; Pred. No. 38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCTGGCAGCAC 20
Db 12 GCTAGCAGCAC 1

RESULT 14
AA31582
ID AAX31582 standard; DNA; 15 BP.
AC AAX31582;
XX
XX 21-MAY-1999 (first entry)
DT
XX
XX Tag sequence of a transcript increased in pancreatic cancer.
DE
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW diagnosis; prognosis; treatment; ss.
XX Homo sapiens.
OS
XX WO9853319-A2.
PN
XX
XX 26-NOV-1998.
PD
XX 20-MAY-1998; 98WO-US010277.
PF
XX 21-MAY-1997; 97US-0047352P.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX
XX Use of isolated gene transcripts - useful for developing products for the
PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX
XX Claim 13; Page 62; 120pp; English.
PS
XX
XX AAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic cancer, or
CC in both. The tag sequences can be used to identify genes by matching the
CC tag to a gen data base member, or by using the tag sequences as probes to
CC isolate unidentified genes from cDNA libraries. The tag sequences can
CC also be used in a method for diagnosing colon or pancreatic cancer in a
CC sample suspected of being neoplastic. The method comprises comparing the
CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.
CC The transcript is identified by a tag selected from AAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer
XX
SQ Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 45;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCGCTG 12
Db 2 ATGGACTCTCTG 13

RESULT 15
ABK32536
ID ABK32536 standard; DNA; 15 BP.
XX
XX AC ABK32536;

XX 23-APR-2002 (first entry)
DT
XX Human pancreatic cancer SAGE tag #88.
DE
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
XX Homo sapiens.
OS
XX US6333152-B1.
PN
XX 25-DEC-2001.
PD
XX 20-MAY-1998; 98US-00081646.
PF
XX 20-MAY-1998; 98US-00081646.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
PT
XX Disclosure; Col 73; 161pp; English.
PS
XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
SQ Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 45;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCGCTG 12
Db 2 ATGGACTCTCTG 13

RESULT 16
AAI71593/c
ID AAI71593 standard; DNA; 16 BP.
XX
AC AAI71593;
XX
XX 10-JAN-2002 (first entry)
DT
XX
XX Lambda vector based cloning system adaptor sequence Sfi-B.
DE
XX Lambda vector; cloning system; homologous recombination; eukaryote;
KW embryonal stem cell; adaptor; ds.
XX
XX Synthetic.
OS
XX DE10016523-A1.
PN
XX 04-OCT-2001.
PD
XX 03-APR-2000; 2000DE-01016523.
PF
XX 03-APR-2000; 2000DE-01016523.
PR
XX (INGE-) INGENIUM PHARM AG.
PA

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XX Nehls M, Wattler S;
PI WPI; 2001-657561/76.
DR
XX
XX Cloning system for homologous recombination, useful for introducing
PT mutations into eukaryotic genomes at selected sites, comprises lambda
PT vector and adaptors.
PT
XX
XX Disclosure; Page 4; 11pp; German.
XX
XX The present invention describes a cloning system useful for homologous
CC recombination in eukaryotic cells and consisting of a vector-adaptor
CC system with a lambda vector and 4 adaptor nucleotides. This can be used
CC to alter the genome of eukaryotic cells, particularly embryonal stem
CC cells, at a desired location. The present sequence is an adaptor sequence
CC used in the construction of the lambda vector of the invention
XX
XX Sequence 16 BP; 3 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
SQ
Query Match 52.0%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 47;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
DB 16 GGCCCTCGCTGGC 5

RESULT 17
AA09136
ID AA09136 standard; DNA; 15 BP.
XX
AC AA09136;
XX
XX 24-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic marker upstream primer #16.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
KW treatment; marker; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9820165-A2.
XX
XX 14-MAY-1998.
XX
XX 05-NOV-1997; 97WO-US020313.
XX
XX 06-NOV-1996; 96US-0030455P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Lander ES, Wang D, Hudson T;
XX
XX WPI; 1998-286974/25.
XX
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
XX Claim 15; Page 48; 310pp; English.
XX
XX AA09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AA091269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular

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CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
XX Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 16
DB 1 TGGCCCTCGCTGCTC 15

RESULT 18
AA045238
ID AA045238 standard; DNA; 15 BP.
XX
AC AA045238;
XX
XX 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #77.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiac; viricide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO2000078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense

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CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGCAGC 20
|||||
DB 1 CTCGCTGGCAGCAGC 15

RESULT 19
AAF73837
ID AAF73837 standard; DNA; 15 BP.
XX
AC AAF73837;
XX
DT 30-APR-2001 (first entry)
XX
DE Human SLC6A4 allele-specific oligonucleotide probe #19.
XX
KW Solute carrier family 6 neurotransmitter transporter; section 4; SLC6A4;
KW genotyping; allele specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200109161-A1.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000WO-US020638.
XX
PR 29-JUL-1999; 99US-0146290P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
DR WPI; 2001-123317/13.
XX
PT New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
PT gene for identifying drugs for treating disorders related to expression
PT of the protein.
XX
PS Claim 12; Page 19; 152pp; English.
XX
CC The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter transporter,
CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
CC complementary to the first sequence. The invention is used in producing a
CC recombinant organism that can be used to express SLC6A4 for protein
CC structure analysis and binding studies. A composition comprising a
CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
CC gene
XX
SQ Sequence 15 BP; 3 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 51.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGACTCTGTCGACG 17
|||||

Db 1 GGAGTTGCTGCGAAG 15

RESULT 20
ACD66350
ID ACD66350 standard; RNA; 15 BP.
XX
AC ACD66350;
XX
DT 23-SEP-2003 (first entry)
XX
DE Anti-HCV nucleic acid molecule target sequence #233.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; anti-HCV;
KW viral replication; degenerative; disease state; HBV infection;
KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
KW hepatotropic; cytostatic; virucide; antiinflammatory; target; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 322; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a target for one of the anti-

CC HCV nucleic acid molecules disclosed in the present invention
 XX
 SQ Sequence 15 BP; 2 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 51.0%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 73.3%; Pred. No. 50;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACTCGCTGGCAGC 18
 |||:|||||
 Db 1 GACUCGUAGGCUCC 15

RESULT 21

ACD66420
 ID ACD66420 standard; RNA; 15 BP.

XX AC ACD66420;

DT 23-SEP-2003 (first entry)

DE Anti-HCV enzymatic nucleic acid substrate sequence #6.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; anti-HCV;
 KW viral replication; degenerative; disease state; HBV infection;
 KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
 KW hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.

XX PN WO200281494-A1.

XX PD 17-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009187.

XX PR 26-MAR-2001; 2001US-00817879.

XX PR 08-JUN-2001; 2001US-00877478.

XX PR 08-JUN-2001; 2001US-0296878P.

XX PR 24-OCT-2001; 2001US-0335059P.

XX PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Claim 1; Page 326; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the
 CC anti-HCV enzymatic nucleic acid sequences disclosed in the present
 CC invention

XX SQ Sequence 15 BP; 2 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 51.0%; Score 10.2; DB 1; Length 15;

Best Local Similarity 73.3%; Pred. No. 50;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACTCGCTGGCAGC 18
 |||:|||||

Db 1 GACUCGUAGGCUCC 15

RESULT 22

ABV71331

ID ABV71331 standard; cDNA; 11 BP.

XX AC ABV71331;

DT 21-OCT-2002 (first entry)

XX Human skin EST 9117.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;

KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

XX WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining

PT homeostasis and identifying cosmetic or pharmaceutical agents against

PT e.g. skin cancer.

XX Claim 24; Page 293; 1345pp; German.

XX The invention relates to in vitro identification (MI) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)

CC so as to identify skin-expressed genes and quantify their expression.

CC (MI) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention

SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TGGCAGCGCAC 20
Db 2 TGGCAGCGCAC 11
RESULT 23
ABV63910
ID ABV63910 standard; cDNA; 11 BP.
XX AC ABV63910;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 1696.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN W0200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX PS Disclosure; Page 71; 1345pp; German.
XX CC The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TGGCAGCGCAC 20
Db 2 TGGCAGCGCAC 11
RESULT 24
ACA61749

ID ACA61749 standard; DNA; 12 BP.
XX AC ACA61749;
XX DT 20-AUG-2003 (first entry)
XX DE Sample preparation and multiplex detection apparatus DNA #9.
XX KW Multiplex detection; ss; spacer element; three dimensional capture probe.
XX OS Unidentified.
XX PN US2003032029-A1.
XX PD 13-FEB-2003.
XX PF 12-MAR-2002; 2002US-00096718.
XX PR 21-DEC-1998; 98US-00217472.
XX PA (NANO-) NANOGEN INC.
XX PI Collins ML;
XX DR WPI; 2003-466222/44.
XX PT Apparatus for carrying out sample preparation and detection of panels of
PT target nucleic acids and antigens in a sample, has sample preparation
PT zone, three dimensional capture probe platforms and spacer elements.
XX PS Example 1; Page 9; 41pp; English.
XX CC The invention relates to an apparatus for carrying out sample preparation
CC and multiplex detection of panels of target nucleic acids and antigens in
CC a sample, comprising a sample preparation zone, several three dimensional
CC capture probe platforms for capturing specific classes of target
CC molecules and spacer elements for separating the sets of three
CC dimensional capture probe platforms. The apparatus is useful for carrying
CC out multiplex detection of panels of target nucleic acids and antigens in
CC a sample, by providing a sample containing target nucleic acids and/or
CC antigens of interest, treating the sample with a sample buffer to form a
CC pre-processed sample, passing the pre-processed sample over the
CC apparatus, capturing the target nucleic acids and antigens by capture
CC probes of the apparatus, reacting a label with a signal probe, the signal
CC probe having specificity for at least one other signal probe, that is
CC specific for the target and detecting the reacted level. Sequences
CC ACA61741-ACA61800 and ACD17023-ACD17041 represent DNA molecules used in
CC the scope of the invention
XX
SQ Sequence 12 BP; 2 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TGGCAGCGCAC 20
Db 2 TGGCAGCGCAC 11
RESULT 25
ACA61769/C
ID ACA61769 standard; DNA; 12 BP.
XX AC ACA61769;
XX DT 20-AUG-2003 (first entry)
XX DE Sample preparation and multiplex detection apparatus DNA #29.
XX KW Multiplex detection; ss; spacer element; three dimensional capture probe.
XX OS Unidentified.

XX US2003032029-A1.
PN
XX 13-FEB-2003.
XX
XX 12-MAR-2002; 2002US-00096718.
XX
XX 21-DEC-1998; 98US-00217472.
XX
XX (NANO-) NANOGEN INC.
PA
XX Collins ML;
PI
XX WPI; 2003-466222/44.
DR
XX
XX Apparatus for carrying out sample preparation and detection of panels of
PT target nucleic acids and antigens in a sample, has sample preparation
PT zone, three dimensional capture probe platforms and spacer elements.
PT
XX Disclosure; Page 19; 41pp; English.
XX
XX The invention relates to an apparatus for carrying out sample preparation
CC and multiplex detection of panels of target nucleic acids and antigens in
CC a sample, comprising a sample preparation zone, several three dimensional
CC capture probe platforms for capturing specific classes of target
CC molecules and spacer elements for separating the sets of three
CC dimensional capture probe platforms. The apparatus is useful for carrying
CC out multiplex detection of panels of target nucleic acids and antigens in
CC a sample, by providing a sample containing target nucleic acids and/or
CC antigens of interest, treating the sample with a sample buffer to form a
CC pre-processed sample, passing the pre-processed sample over the
CC apparatus, capturing the target nucleic acids and antigens by capture
CC probes of the apparatus, reacting a label with a signal probe, the signal
CC probe having specificity for at least one other signal probe that is
CC specific for the target and detecting the reacted level. Sequences
CC ACA61741-ACA61800 and ACD17023-ACD17041 represent DNA molecules used in
CC the scope of the invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGSCACGCAC 20
Db 11 TGSCACGCAC 2
|||||||
|||:|||||

RESULT 26
AAT49691
ID AAT49691 standard; RNA; 15 BP.
XX
XX AAT49691;
AC
XX
XX 02-MAR-1997 (first entry)
DT
XX
XX Human CPTP HH ribozyme target sequence #996.
DE
XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CPTP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
XX Homo sapiens.
OS
XX WO9620279-A1.
FN
XX
XX 04-JUL-1996.
PD
XX

PF 11-DEC-1995; 95WO-US016000.
XX
XX 23-DEC-1994; 94US-00363240.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
PI
XX WPI; 1996-321852/32.
DR
XX
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
PT
XX Claim 4; Page 30; 72pp; English.
PS
XX AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence UH
CC is immediately upstream. The ribozymes are able to cleave mRNA from the
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels), and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 1 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTGCTGGC 14
Db 5 ACUCGCGGC 14
||:|||||
|||:|||||

RESULT 27
ABX76579
ID ABX76579 standard; DNA; 15 BP.
XX
XX ABX76579;
AC
XX
XX 01-APR-2003 (first entry)
DT
XX
XX M. avium 16S rRNA mutated probe #8.
DE
XX Probe; 23S rRNA; 16SrRNA; tuberculosis; MTC; MOTT; peptide nucleic acid;
KW mycobacterium tuberculosis complex; precursor rRNA; rDNA; SS rRNA; ss;
KW mycobacterium other than tuberculosis; mutant;
KW 16S-mediated streptomycin resistance.
XX
XX Mycobacterium tuberculosis.
OS
XX Synthetic.
XX
XX US2002137035-A1.
FN
XX 26-SEP-2002.
PD

```

XX PF 07-APR-2000; 2000US-00544934.
XX PR 07-APR-2000; 2000US-00544934.
XX PA (STEN/) STENDER H.
XX PA (LUND/) LUND K.
XX PA (MOLL/) MOLLERUP T A.
XX PI Stender H, Lund K, Mollerup TA;
XX DR WPI; 2003-174116/17.
XX PT Peptide nucleic acid probes for detecting target sequences of
XX PT Mycobacteria in samples, e.g., sputum, which are capable of hybridizing
XX PT to a target sequence of mycobacterial rDNA, precursor rRNA or rRNA
XX PT forming detectable hybrids.
XX PS Claim 22; Page 40; 74pp; English.
XX CC The invention relates to a peptide nucleic acid capable of hybridizing to
XX CC a target sequence of Mycobacterial rDNA, precursor rRNA or rRNA (5S, 16S
XX CC or 23S) forming detectable hybrids. Also included are detecting a target
XX CC sequence of mycobacteria in a sample comprising contacting rRNA or rDNA
XX CC in the sample with peptide nucleic acid probes (hybridisation takes place
XX CC between the probe and the rRNA or rDNA), observing or measuring any
XX CC formed detectable hybrids and relating the observation or measurement to
XX CC the presence of a target sequence of mycobacteria in the sample, and a
XX CC kit for detecting a target sequence of mycobacteria in particular a
XX CC target sequence of mycobacteria of M. tuberculosis complex (MTC). The
XX CC probes are used for detecting a target sequence of MTC (and
XX CC distinguishing them from mycobacterium other than tuberculosis, MOTT)
XX CC present in a sample, e.g. sputum, laryngeal swabs, gastric lavage,
XX CC bronchial washings, biopsies, aspirates, expectorates, body fluids,
XX CC urine, tissue sections as well as food samples, soil, air and water
XX CC samples and their cultures. The probe is able to penetrate the cell wall
XX CC of the mycobacteria. It is able to hybridise to Mycobacterial precursor
XX CC rRNA and rRNA without harsh treatment of the mycobacterial cells.
XX CC therefore avoiding a risk of interfering with the morphology of the
XX CC cells. The present sequence is a mutant M. tuberculosis probe for 16S
XX CC rRNA around position 473-477, associated with 16S-mediated streptomycin
XX CC resistance
XX SQ Sequence 15 BP; 1 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CGCTGGCAAG 17
Db 5 CGCTGGCAAG 14

RESULT 28
AAT49650/c
ID AAT49650 standard; RNA; 15 BP.
XX AC AAT49650;
XX XX
DT 28-FEB-1997 (first entry)
XX XX
DE Human CERP HH ribozyme target sequence #286.
XX XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetaipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX OS Homo sapiens.

XX PF 07-APR-2000; 2000US-00544934.
XX PR 07-APR-2000; 2000US-00544934.
XX PA (STEN/) STENDER H.
XX PA (LUND/) LUND K.
XX PA (MOLL/) MOLLERUP T A.
XX PI Stender H, Lund K, Mollerup TA;
XX DR WPI; 2003-174116/17.
XX PT Peptide nucleic acid probes for detecting target sequences of
XX PT Mycobacteria in samples, e.g., sputum, which are capable of hybridizing
XX PT to a target sequence of mycobacterial rDNA, precursor rRNA or rRNA
XX PT forming detectable hybrids.
XX PS Claim 22; Page 40; 74pp; English.
XX CC The invention relates to a peptide nucleic acid capable of hybridizing to
XX CC a target sequence of Mycobacterial rDNA, precursor rRNA or rRNA (5S, 16S
XX CC or 23S) forming detectable hybrids. Also included are detecting a target
XX CC sequence of mycobacteria in a sample comprising contacting rRNA or rDNA
XX CC in the sample with peptide nucleic acid probes (hybridisation takes place
XX CC between the probe and the rRNA or rDNA), observing or measuring any
XX CC formed detectable hybrids and relating the observation or measurement to
XX CC the presence of a target sequence of mycobacteria in the sample, and a
XX CC kit for detecting a target sequence of mycobacteria in particular a
XX CC target sequence of mycobacteria of M. tuberculosis complex (MTC). The
XX CC probes are used for detecting a target sequence of MTC (and
XX CC distinguishing them from mycobacterium other than tuberculosis, MOTT)
XX CC present in a sample, e.g. sputum, laryngeal swabs, gastric lavage,
XX CC bronchial washings, biopsies, aspirates, expectorates, body fluids,
XX CC urine, tissue sections as well as food samples, soil, air and water
XX CC samples and their cultures. The probe is able to penetrate the cell wall
XX CC of the mycobacteria. It is able to hybridise to Mycobacterial precursor
XX CC rRNA and rRNA without harsh treatment of the mycobacterial cells.
XX CC therefore avoiding a risk of interfering with the morphology of the
XX CC cells. The present sequence is a mutant M. tuberculosis probe for 16S
XX CC rRNA around position 473-477, associated with 16S-mediated streptomycin
XX CC resistance
XX SQ Sequence 15 BP; 1 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CGCTGGCAAG 17
Db 5 CGCTGGCAAG 14

RESULT 28
AAT49650/c
ID AAT49650 standard; RNA; 15 BP.
XX AC AAT49650;
XX XX
DT 28-FEB-1997 (first entry)
XX XX
DE Human CERP HH ribozyme target sequence #286.
XX XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetaipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX OS Homo sapiens.

XX PN WO9620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (WARN) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX DR WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX PT useful for preventing or treating initial development, progression or
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 30; 72pp; English.
XX CC AAT49608-749863 represent target sequences for the human cholesterol
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX CC transfer between plasma lipoproteins. The numbering of the targets refers
XX CC to the position of the cleavage site in full length CETP. The ribozyme UH
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size
XX CC density of the high density lipoproteins (HDL), prolonging HDL half life,
XX CC and therefore increasing HDL levels. The ribozymes can be used to treat
XX CC conditions associated with abnormal levels of CETP, specifically familial
XX CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX CC hypoalphalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
XX CC vascular complications of diabetes, transplant, atherectomy and
XX CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX CC The HH ribozymes can also be used diagnostically to study genetic drift
XX CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX CC ribozymes target specific regions of the CETP gene, they have low non-
XX CC specific activity
XX SQ Sequence 15 BP; 2 A; 7 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CTCGCTGGCAAGC 18
Db 15 CTCGCTGGCAAGC 3

RESULT 29
AAT70096
ID AAT70096 standard; DNA; 15 BP.
XX AC AAT70096;
XX XX
DT 15-SEP-1997 (first entry)
XX XX
DE Primer NGFTE-4 used to construct vector to express neurotrophin-3.
XX NT-3; neurotrophin 3; active; refolded; differentiation; research; human;
KW expression; protein induction; enzyme expression; primer; PCR; ss.
XX Synthetic.
XX OS Homo sapiens.
XX PN JP09121886-A.

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XX 13-MAY-1997.
 XX 22-AUG-1996; 96JP-00220963.
 XX 25-AUG-1995; 95JP-00217032.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX WPI; 1997-314237/29.
 XX Preparation of active correctly folded neurotrophin-3 - which can be used
 PT in cell differentiation, and protein expression research.
 XX Disclosure; Page 7; 15pp; Japanese.
 XX AAT70094-96 are primers used to construct a vector capable of expressing
 CC human neurotrophin 3 (NT-3). Active NT-3 is produced by the method of the
 CC invention, which comprises transforming a prokaryotic host cell with an
 CC NT-3 gene to express the NT-3, and then NT-3 produced is refolded
 CC correctly in a redox buffer. The active NT-3 produced by the method can
 CC be used as a reagent for research on the differentiation of cells,
 CC genetic expression and induction of protein and enzyme expression
 XX Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 TCGCTGGCAGCA 19
 |||||
 DB 3 TCCTGGCATGCA 15
 RESULT 30
 AAT80039
 ID AAT80039 standard; cDNA; 15 BP.
 XX AAT80039;
 XX 29-OCT-1997 (first entry)
 XX Alpha2 integrin primer #4.
 XX PCR; polymerase chain reaction; primer; amplify; alpha integrin;
 KW alpha2 integrin; glomerulopathy; diabetes; nephropathy; ss.
 XX Synthetic.
 XX WO9704133-A1.
 XX 06-FEB-1997.
 XX 19-JUL-1996; 96WO-US012067.
 XX 21-JUL-1995; 95US-0001387P.
 XX 03-AUG-1995; 95US-0001861P.
 XX 02-MAY-1996; 96US-0016700P.
 XX (MINU) UNIV MINNESOTA.
 XX Tailibary P, Charonis AS, Setty S, Mauer M;
 XX WPI; 1997-132668/12.
 XX Detection of nephropathy in mammals - by comparing integrin subunit
 PT expression in a tissue sample compared to a control tissue sample.
 XX Example 6; Page 35; 73pp; English.
 XX AAT80036-T80041 represent amplification primers for the alpha2 integrin
 CC coding sequence. The primers represented in AAT80030-T80035 are used for

CC the amplification of the alpha1 integrin coding sequence. These sequences
 CC can be used in the method of the invention. The method of the invention
 CC is for the identification of a mammal having, or at risk of developing,
 CC glomerulopathy. The method comprises analysing a tissue sample from a
 CC mammal known to contain cells expressing integrin RNA or protein in the
 CC integrin subunit expression. The integrin subunit expression in the
 CC sample is then compared with a control tissue sample, where altered
 CC integrin subunit expression is correlated with glomerulopathy. The method
 CC can be modified to identify a mammal with diabetes who has, or is at risk
 CC of developing, secondary pathological changes associated with diabetes.
 CC An increase in alpha2,3,5 or beta-1 integrin expression and/or a decrease
 CC in alpha1 expression is diagnostic of increased risk of nephropathy. The
 CC methods can be used to determine if patients are likely to develop severe
 CC nephropathy and to monitor progress of disease during treatment protocols
 XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGGACTCGCTGG 13
 |||||
 DB 3 ATGTACTCACTGG 15
 RESULT 31
 AAX75739
 ID AAX75739 standard; RNA; 15 BP.
 XX AAX75739;
 XX 28-JUL-1999 (first entry)
 XX Human flt-1 and KDR hammerhead ribozyme target site #73.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX Homo sapiens.
 XX WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 XX 11-JAN-1996; 96US-00584040.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Example 9; Page 192; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

CC	treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
XX	
SQ	Sequence 15 BP; 3 A; 2 C; 5 G; 0 T; 5 U; 0 Other;
Query Match	49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity	61.5%; Pred. No. 61;
Matches	8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY	1 ATGGACTCGTGG 13 : : : : :
Db	1 AUGGAACUCUGG 13 : : : : :
RESULT 32	
AAI67291/c	
ID	AAI67291 standard; DNA; 15 BP.
XX	
AC	AAI67291;
XX	
DT	11-FEB-2002 (first entry)
DE	
DE	Human FKBP8 allele-specific oligonucleotide (ASO) probe.
KW	FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer; ss;
KW	immunosuppression; human; allele-specific oligonucleotide; ASO; probe.
OS	Homo sapiens.
FN	WO200172965-A2.
XX	
PD	04-OCT-2001.
XX	
PF	26-MAR-2001; 2001WO-US009718.
XX	
PR	24-MAR-2000; 2000US-019212SP.
XX	
PA	(GENA-) GENAISSANCE PHARM INC.
XX	
PI	Anastasio AE, Bentivegna SC, Choi JY, Kliehm SE, Koshy B;
PI	Stephens JC;
XX	
DR	WPI; 2001-626261/72.
XX	
PT	New haplotypes of the FK506-binding protein 8 gene, useful for genotyping that gene in individual and to design new therapy for associated disease such as immunosuppression and cancer.
PS	Claim 15; Page 13; 98pp; English.
XX	
CC	The invention relates to haplotyping the FK506-binding protein 8 (38kd) (FKBP8) gene in an individual. The method involves determining the identity of the nucleotide pair at one or more polymorphic sites selected from P1 to P26 (described in the specification). The invention is useful to improve the efficiency and reliability of several steps in the CC discovery and development of drugs for treating diseases associated with FKBP8 activity, for example immunosuppression and cancer. Sequences CC AAI67274-299 represent allele-specific oligonucleotide (ASO) probes for detecting FKBP8 gene polymorphisms
XX	
SQ	Sequence 15 BP; 0 A; 3 C; 8 G; 3 T; 0 U; 1 Other;
Query Match	49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity	73.3%; Pred. No. 61;
Matches	11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY	4 GACTCGTCGCAGC 18 :: : :
Db	15 GACACCCYGCCACC 1 :: : :
RESULT 33	

XX 30-MAR-2001 (first entry)
 DT IGFBP2 oligonucleotide #79.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI
 XX WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 CTCGCTCGCACGC 18
 Db 3 CTCGCTCGCCGC 15
 |||||
 RESULT 35
 AAF45957
 ID AAF45957 standard; DNA; 15 BP.
 XX
 AC AAF45957;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGFBP2 oligonucleotide #796.
 DE

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI
 XX WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 39; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 4 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 GGACTCGCTGGCA 15
 Db 2 GGACTCCCTGCCA 14
 |||||
 RESULT 36
 AAF45236
 ID AAF45236 standard; DNA; 15 BP.
 XX
 AC AAF45236;
 XX
 XX 30-MAR-2001 (first entry)
 DT
 XX IGFBP2 oligonucleotide #75.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW

IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 hyperneovascular condition; hyperplasia; kidney disease;
 neovascular condition of the retina; ss.

OS Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 inhibits or reduces growth factor mediated cell proliferation and/or
 inflammation.

PS Example 6; Page 34; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 inhibiting or reducing growth factor mediated cell proliferation,
 inflammation and/or other disorders. The present sequence is an
 oligonucleotide which can be used to design the antisense
 oligonucleotides of the present invention (see AAF45151 and AAF45153-
 F45161). The method is useful for ameliorating the effects of psoriasis,
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 neoplasia, scleroderma, warts, benign growths, cancers of the skin, a
 hyperneovascular condition such as a neovascular condition of the retina,
 brain or skin, growth factor-mediated malignancies, other sclerotic
 disease, kidney disease, hyperproliferation of the inside of blood
 vessels or any other hyperplasia

XX Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 CTCGCTGGCAGC 18
 Db 3 CTCGCTGGCTCGC 15

RESULT 37
 AAF45242
 ID AAF45242 standard; DNA; 15 BP.

XX AAF45242;

XX 30-MAR-2001 (first entry)

DE IGFBP2 oligonucleotide #81.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 inhibits or reduces growth factor mediated cell proliferation and/or
 inflammation.

XX Example 6; Page 34; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 inhibiting or reducing growth factor mediated cell proliferation,
 inflammation and/or other disorders. The present sequence is an
 oligonucleotide which can be used to design the antisense
 oligonucleotides of the present invention (see AAF45151 and AAF45153-
 F45161). The method is useful for ameliorating the effects of psoriasis,
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 neoplasia, scleroderma, warts, benign growths, cancers of the skin, a
 hyperneovascular condition such as a neovascular condition of the retina,
 brain or skin, growth factor-mediated malignancies, other sclerotic
 disease, kidney disease, hyperproliferation of the inside of blood
 vessels or any other hyperplasia

XX Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 CTCGCTGGCAGC 18
 Db 1 CTCGCTGGCTCGC 13

RESULT 38

AAF45237

ID AAF45237 standard; DNA; 15 BP.

XX AAF45237;

XX 30-MAR-2001 (first entry)

DE IGFBP2 oligonucleotide #76.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 hyperneovascular condition; hyperplasia; kidney disease;
 neovascular condition of the retina; ss.

OS Homo sapiens.

XX

PN WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAGC 18
 DB ||||| |||||
 2 CTCGCTGGCTCGC 14
 RESULT 39
 AAF45241
 ID AAF45241 standard; DNA; 15 BP.
 XX AAF45241;
 XX 30-MAR-2001 (first entry)
 XX IGFBP2 oligonucleotide #80.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAGC 18
 DB ||||| |||||
 2 CTCGCTGGCTCGC 14
 RESULT 40
 AAF45956
 ID AAF45956 standard; DNA; 15 BP.
 XX AAF45956;
 XX 30-MAR-2001 (first entry)
 XX IGFBP2 oligonucleotide #795.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAGC 18
 DB ||||| |||||
 2 CTCGCTGGCTCGC 14

PF 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAGC 18
 DB ||||| |||||
 2 CTCGCTGGCTCGC 14
 RESULT 40
 AAF45956
 ID AAF45956 standard; DNA; 15 BP.
 XX AAF45956;
 XX 30-MAR-2001 (first entry)
 XX IGFBP2 oligonucleotide #795.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 6; Page 34; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAGC 18
 DB ||||| |||||
 2 CTCGCTGGCTCGC 14

PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX
 PS Example 6; Page 39; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisenescence
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC R45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 XX
 SQ Sequence 15 BP; 3 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GGACTCGCTGCCA 15
 DB 3 GGACTCCCTGCCA 15
 RESULT 41
 ABL95817
 ID ABL95817 standard; DNA; 15 BP.
 XX
 AC ABL95817;
 XX
 XX 19-JUN-2002 (first entry)
 XX
 DE Myeloid progenitor inhibitory factor-1delta23 oligonucleotide #31.
 XX
 KW Recombinant protein production; drug; reagent; food stuff; ss.
 XX
 OS Unidentified.
 XX
 XX WO200208417-A1.
 PN
 XX 31-JAN-2002.
 PD
 XX 25-JUL-2001; 2001WO-JP006392.
 PF
 XX 25-JUL-2000; 2000JP-00229064.
 PR
 XX (TAKEDA) TAKEDA CHEM IND LTD.
 PA
 PI Ito T, Tanaka Y, Kondo M;
 XX
 XX WPI; 2002-179906/23.
 DR
 XX Production of recombinant proteins in prokaryotes or eukaryotes
 PT particularly with target proteins obtainable through gene recombination
 PT technique, for use as drugs, reagents, raw materials for industries and
 PT feeding stuffs.
 XX
 XX

PS Example 6; Page 42; 137pp; Japanese.
 XX
 CC The present invention relates to a method for producing recombinant
 CC proteins. The method comprises preparing a recombinant vector for
 CC transforming a host cell before culturing the obtained transformant,
 CC assaying expression of the reporter gene and confirming high expression
 CC of the reporter gene. The recombinant proteins are useful as drugs,
 CC reagents, raw materials for industries and feeding stuffs. Also, the
 CC proteins are obtainable on large-scale production. The present sequence
 CC was used to illustrate the invention
 XX
 XX Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 61;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 TCGCTGGCAGCA 19
 DB 3 TCGCTCCACGCA 15
 RESULT 42
 ABL95310/c
 ID ABL95310 standard; DNA; 15 BP.
 XX
 AC ABL95310;
 XX
 XX 24-OCT-2002 (first entry)
 DT
 XX Human N-acetylgalactosaminidase (NAGA) alpha gene ASO primer 2.
 DE
 XX Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
 KW chromosome 22q13.2-q13.31; lysosomal glycosidase; screening; SNP;
 KW NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
 KW genotyping.
 XX
 OS Homo sapiens.
 XX
 XX WO200194637-A1.
 PN
 XX 13-DEC-2001.
 PD
 XX 07-JUN-2001; 2001WO-US018456.
 PF
 XX 07-JUN-2000; 2000US-0210110P.
 PR
 XX (GENA-) GENAISANCE PHARM INC.
 PA
 PI Duda A, Kazemi A, Koshy B, Parks KE;
 XX
 XX WPI; 2002-566449/60.
 DR
 XX New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
 PT gene, useful for therapeutic purposes, for studying the expression and
 PT function of the polynucleotide, and for expressing NAGA protein.
 XX
 XX Claim 16; Page 13; 91pp; English.
 PS
 XX The invention comprises the amino acid and coding sequence of the human N
 CC -acetylgalactosaminidase (NAGA) alpha protein. The invention specifically
 CC comprises novel polymorphic sites identified within the NAGA gene. The
 CC NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a
 CC lysosomal glycosidase that cleaves alpha-N-acetylgalactosaminyl
 CC moieties in glycoconjugates. The NAGA DNA and protein sequences of the
 CC invention are useful for studying the expression and function of NAGA and
 CC for screening candidate drugs to treat diseases related to NAGA activity.
 CC The NAGA gene polymorphisms identified in the present invention are
 CC useful for haplotyping and genotyping the NAGA gene of an individual. The
 CC present DNA sequence represents an N-acetylgalactosaminidase gene allele-
 CC specific oligonucleotide primer
 XX
 XX Sequence 15 BP; 2 A; 3 C; 7 G; 2 T; 0 U; 1 Other;
 SQ

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGCAC 16
| | | | | | | | | |
DB 13 GCTCGCTAGCAC 1

RESULT 43
ABS59479/C
ID ABS59479 standard; RNA; 15 BP.

XX AC ABS59479;

XX DT 05-NOV-2002 (first entry)

XX DE RNA sequence #5, for sample identification.

XX KW Genetic affinity; virus; genetic relative; node; bifurcating tree; ss;
XX KW genetic relationship; signature probe; phylogenetic affinity;
XX KW space flight; medicine; indoor air quality; bioaerosol; mass destruction;
XX KW epidemic; phylogenetic tree; air filtrate; government building;
XX KW bioterrorism agent; molecular beacon; bacteria; Bacillus; Kohne approach.

XX OS Isosphaera sp.

XX PN WO200259348-A2.

XX PD 01-AUG-2002.

XX PF 26-JAN-2002; 2002WO-US0002564.

XX PR 26-JAN-2001; 2001US-0264403P.

XX PA (TECH-) TECHNOLOGY LICENSING CO LLC.

XX PI Fox GE, Wilson RC, Zhang Z;

XX DR WPI; 2002-619174/66.

XX PT Determining the genetic affinity of organisms or viruses useful in
XX PT bioterrorism, comprises determining which nodes in the bifurcating tree
XX PT of genetic relationship that designs the signature probes produces the
XX PT hybridization signal.

XX PS Claim 17; Page 36; 62pp; English.

XX CC The present invention relates to a new method for determining the genetic
XX CC affinity of organisms or viruses in the test sample. The method involves
XX CC identifying the closest known genetic relatives of the organisms or virus
XX CC by determining which nodes in the bifurcating tree of genetic
XX CC relationship was used to design the signature probes. The method is
XX CC useful in identifying the phylogenetic affinity of an unknown organism
XX CC useful for unanticipated problems involving microorganisms that concerns
XX CC space flight, medicine, indoor air quality, bioaerosols of mass
XX CC destruction, or epidemics. The signature sequences are useful in the
XX CC hybridisation to determine the phylogenetic tree positions of the
XX CC organisms in the sample. The method can also be useful as an assay for
XX CC bioterrorism. Air filtrate from a government building was collected and
XX CC nucleic acids isolated. RNA was enriched using DNase and RNA fragmented
XX CC by heating. Probes specific to several known bioterrorism agents give
XX CC negative results. Molecular beacon based scoring of signature sequences
XX CC reveals the presence of unexpectedly high concentrations of bacteria with
XX CC genetic affinity to genus Bacillus. The method provides a more rapid
XX CC approach for determining the affinity of organisms in the test sample.
XX CC The methodology is more general than the specifically targeted tests of
XX CC the Kohne approach, and faster and more convenient than detailed
XX CC sequencing of the RNAs or their encoding DNA. The present nucleic acid
XX CC sequence represents an RNA sequence that was used in the methods of the
XX CC invention for sample identification

SQ Sequence 15 BP; 1 A; 3 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGC 18
| | | | | | | | | |
DB 14 CAGCGCTGCAGC 2

RESULT 44

ABQ80146
ID ABQ80146 standard; DNA; 15 BP.

XX AC ABQ80146;

XX DT 13-JUN-2003 (first entry)

XX DE Left primer DBM0112B amplifies IL4R amplicon of 177 bp.

XX KW Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele;
XX KW insulin dependent diabetes mellitus; IDDM; myasthenia gravis; PCR;
XX KW single nucleotide polymorphism; SNP; autoimmune disease; amplify;
XX KW T helper type 1 mediated disease; rheumatoid arthritis; primer;
XX KW multiple sclerosis; inflammatory bowel disease; systemic sclerosis;
XX KW systemic lupus erythematosus; psoriasis; scleroderma; Grave's disease;
XX KW Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.

XX OS Homo sapiens.

XX PN WO2003010335-A2.

XX PD 06-FEB-2003.

XX PF 17-JUL-2002; 2002WO-EP007956.

XX PR 20-JUL-2001; 2001US-0306912P.

XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Mirel DB, Erlich HA, Bugawan TL, Noble JA, Valdez AM;

XX DR WPI; 2003-248086/24.

XX PT Determining an individual's risk for type 1 diabetes, comprises detecting
XX PT the presence of an insulin dependent diabetes mellitus-associated
XX PT interleukin 4 receptor allele in a nucleic acid sample of the individual.

XX CC Example 4; Page 35; 79pp; English.

XX CC The sequences given in ABQ80141-52 represent primers which were used to
XX CC identify wild type and variant loci in the human interleukin 4 receptor
XX CC (IL4R). These primer sequences were used in the method of the invention
XX CC for determining an individual's risk for type 1 diabetes. The method
XX CC comprises detecting the presence of an insulin dependent diabetes
XX CC mellitus (IDDM)-associated interleukin 4 receptor allele in a nucleic
XX CC acid sample of the individual, where the presence of the allele indicates
XX CC the individual's risk for type 1 diabetes. The method identifies one or
XX CC more single nucleotide polymorphism (SNP) within the IL4R gene listed in
XX CC the specification. The method and the SNP's are useful for determining an
XX CC individual's risk for type 1 diabetes. The IL4R SNP's are also useful for
XX CC determining an individual's risk for any autoimmune disease or condition,
XX CC or any T helper type 1 mediated disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, inflammatory bowel disease, systemic lupus
XX CC erythematosus, psoriasis, scleroderma, Grave's disease, systemic
XX CC sclerosis, myasthenia gravis, Guillain-Barre syndrome, or Hashimoto's
XX CC thyroiditis

SQ Sequence 15 BP; 1 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 15;


```

XX PF 26-SEP-1997; 97WO-EP005290.
XX PR 27-SEP-1996; 96GB-00020216.
XX PA (SANG-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX PI Consalez G, Pesce R;
XX DR WPI; 1998-230725/20.
XX
XX PT Differential screening of gene expression by reverse transcription
XX PT polymerase chain reaction - uses random priming with primers selected for
XX PT high efficiency and selectivity by computer screening of database(s).
XX PS Claim 9; Page 24; 37pp; English.
XX
XX CC The invention provides a method for the differential screening of gene
XX CC expression by random primed reverse transcription PCR (RT-PCR). The
XX CC primer sequences are generated by stimulating PCR reactions on non-
XX CC redundant mammalian nucleotide sequence databank entries containing at
XX CC least 1,000 bp of coding region. The primers selected, such as the
XX CC present one, had to meet various criteria such as having an efficiency
XX CC index between 2-10, having a selectivity index higher than 1, being 12 bp
XX CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others
XX CC in at least 5 of the 8 bases at the 3'-end. The invention claims the
XX CC selected primers make it possible to use internally primed, PCR-based RNA
XX CC fingerprinting for simple, exhaustive and systematic analysis of
XX CC differential gene expression as an advantageous alternative to
XX CC differential display. The method can also be useful for isolating new
XX CC coding sequences and to compare known and new genes
XX
XX SQ Sequence 12 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 1 Other;
      Query Match 47.0%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred. No. 64;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 3 GGACTCGTGG 13
XX Db 11 GGACTCGTGG 1
XX
XX RESULT 48
XX ID ABC22800/c
XX AC ABC22800 standard; DNA; 13 BP.
XX AC ABC22800;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 22817 for detecting SNP TSC0004487.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide SEQ ID NO 22817 for detecting SNP TSC0004487.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX

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PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 22817; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 1 Other;
      Query Match 47.0%; Score 9.4; DB 1; Length 13;
      Best Local Similarity 76.9%; Pred. No. 68;
      Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 GACTCGTGGCAC 16
XX Db 13 RACTCGCTACAC 1
XX
XX RESULT 49
XX ID ABC22801
XX AC ABC22801 standard; DNA; 13 BP.
XX AC ABC22801;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 22818 for detecting SNP TSC0004487.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 22818; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 1 Other;
Query Match 47.0%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 68;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACTCGCTGGCAC 16
Db 1 RACTCGCTAACAC 13
RESULT 50
AAZ23798
ID AAZ23798 standard; RNA; 14 BP.
XX
AC AAZ23798;
XX
DT 14-JAN-2000 (first entry)
XX
DE HSV RNA fragment 16.
XX
KW Antisense; DNA library; identification; multiple cloning site; MCS;
XX inhibition; ss.
XX Herpes simplex virus unknown type.
XX
XX WO9950457-A1.
XX
XX 07-OCT-1999.
XX
XX 28-MAR-1999; 99WO-US006742.
XX
XX 28-MAR-1998; 98US-0079792P.
XX 06-NOV-1998; 98US-0107504P.
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Ruffner DE, Pierce ML, Chen Z;
XX WPI; 1999-610866/52.
XX
XX Production of antisense libraries, used for identifying antisense agents
XX and for identifying target sites for antisense-mediated inhibition of a
XX selected gene.
XX
XX Example 4; Page 60; 63pp; English.
XX
XX This invention describes a novel method for generating an antisense
XX library targeted to a selected RNA transcript. The methods can be used
XX for identifying antisense agents and for identifying target sites for
XX antisense-mediated inhibition of a selected gene. The use of a direct
XX library for target site selection significantly simplifies the screening
XX process, since only very small libraries need be prepared and assayed.
XX AAZ23783-223798 represent RNA fragments derived from the Herpes simplex
XX virus genome which are used to illustrate the method of the invention
XX
SQ Sequence 14 BP; 1 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 72.7%; Pred. No. 72;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCTGG 13
Db 3 GGAUUCGUGG 13

RESULT 51
ABV99924/c
ID ABV99924 standard; DNA; 14 BP.
XX
AC ABV99924;
XX
DT 24-FEB-2003 (first entry)
XX
DE Oligonucleotide SU1.
XX
KW Viral detection; blood sample; Hepatitis C virus; ss.
XX
OS Unidentified.
XX
XX RU2186388-C2.
XX
XX 27-JUL-2002.
XX
XX 13-JUL-2000; 2000RU-00118422.
XX
XX 13-JUL-2000; 2000RU-00118422.
XX (AMHA=) A MED HAEMATOLOGY RES CENTRE.
XX (SUDA/) SUDARIKOV A B.
XX
XX Glinshchikova OA, Sudarikov AB;
XX
XX WPI; 2002-606525/65.
XX
XX Method for quantitative detection of hepatitis c virus rna in blood
XX serum.
XX
XX Disclosure; Page 3; 5pp; Russian.
XX
XX The invention relates to methods for detecting the quantity of viral
XX genomes in a blood sample. To illustrate the method Hepatitis C viral
XX levels from patient blood serum samples were measured. A retroviral
XX vector, which contained a modified sequence of hepatitis C virus (used as
XX an internal standard for PCR amplification) and a selective marker was
XX used. The suggested retroviral standard was obtained from the culture of
XX packing cells by gathering the cultivation medium where cells were
XX growing. The presence of resistance gene to puromycin in the vector
XX allowed detection of the titer of standard's viral particles in
XX experiments on infecting the cell cultures. The present oligonucleotide
XX was used to illustrate the invention
XX
SQ Sequence 14 BP; 1 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 46.0%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 80;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGACTCGCTGGCAC 16
Db 14 GCATCGCAAGCAC 1
RESULT 52
AAD48184/c
ID AAD48184 standard; DNA; 14 BP.
XX
AC AAD48184;
XX
XX 24-FEB-2003 (first entry)
XX
XX Flu-2 RNA probe used for evaluation of combination oligomers.
XX
XX Peptide nucleic acid; RNA; nucleic acid zygosity; genetic analysis;
XX scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;
XX probe; ss.
XX
XX Unidentified.
XX

CC sequence of contiguous nucleobases in the polynucleobase strand, to form
 CC a double stranded target sequence-oligomer complex. The composition is
 CC used for determining a target sequence of contiguous nucleobases and for
 CC determining the zygosity of a nucleic acid for a single nucleotide
 CC polymorphism (SNP). The methods are useful in scientific investigation,
 CC e.g., for detection, identification and/or enumeration of bacteria,
 CC viruses and pathogens in food, beverages, water, pharmaceutical products,
 CC personal care products, dairy products, in clinical samples or in samples
 CC of plant, animal, human or environmental origin. They are also useful for
 CC the analysis of raw materials, equipment, products or processes used to
 CC manufacture or store food, beverages, water, pharmaceutical products,
 CC personal care products dairy products or environmental samples. The
 CC methods and materials are useful in areas such as expression analysis,
 CC SNP analysis, genetic analysis of humans, animals, fungi, yeast viruses
 CC and plants, therapy monitoring, pharmacogenomics, pharmacogenetics,
 CC epigenomics and high throughput screening operations. The present
 CC sequence is a PNA probe used for evaluation of combination oligomers.
 CC This sequence is used in the exemplification of the invention
 XX

Seq - Sequence 14 BP; 2 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 46.0%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 80;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTCGCTGCACGCA 19
 Db 14 CACGCTGACGTA 1

RESULT 54
 AAD48186/c
 ID AAD48186 standard; DNA; 14 BP.
 XX
 AC AAD48186;
 DT
 DT 24-FEB-2003 (first entry)
 XX
 DE Fluo-4 PNA probe used for evaluation of combination oligomers.
 XX
 KW Peptide nucleic acid; PNA; nucleic acid zygosity; genetic analysis;
 KW scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;
 KW probe; ss.
 XX

OS Unidentified.

Key Location/Qualifiers
 modified_base 1..14
 /*tag= a
 /mod_base= OTHER
 /note= "This sequence is a peptide nucleic acid i.e. it
 contains a polyamide backbone instead of a deoxyribose-
 phosphate backbone"
 modified_base 1
 /*tag= b
 /mod_base= OTHER
 /note= "This base is linked to P-OEE where F, O and E
 represent 5-(6)-carboxyfluorescein, 8-amino-3,6-
 dioxoacetic acid and linker respectively"
 modified_base 7..8
 /*tag= c
 /mod_base= OTHER
 /note= "These bases are linked via Gly-Gly linker"
 modified_base 14
 /*tag= d
 /mod_base= OTHER
 /note= "This base is linked to EB-NH2 group where E
 represents a linker"

PN WO200272865-A2.

XX 19-SEP-2002.

XX

PF 09-MAR-2002; 2002WO-US007050.

XX 09-MAR-2001; 2001US-0274547P.

XX (BOST-) BOSTON PROBES INC.

XX Coull JM, Flandaca MJ, Kristjanson MD, Hyldig-Nielsen JJ;
 PI Creasey TM;

XX WPI; 2003-018741/01.

XX Composition for determining target sequence of contiguous nucleobases,
 PT comprises polynucleobase strand and combination oligomer comprising first
 PT and second oligomer blocks that are covalently linked to each other.

XX Example 3; Page 64; 149pp; English.

XX The present invention relates to combination oligomers, including block
 CC synthesis of combination of oligomers in the absence of a template. The
 CC invention relates to a composition comprising a polynucleobase strand and
 CC a combination oligomer comprising first and second oligomer blocks that
 CC are each independently a peptide nucleic acid (PNA) covalently linked to
 CC each other by a linker of at least three atoms in length, where the
 CC oligomer blocks are sequences specifically hybridised to a target
 CC sequence of contiguous nucleobases in the polynucleobase strand, to form
 CC a double stranded target sequence-oligomer complex. The composition is
 CC used for determining a target sequence of contiguous nucleobases and for
 CC determining the zygosity of a nucleic acid for a single nucleotide
 CC polymorphism (SNP). The methods are useful in scientific investigation,
 CC e.g., for detection, identification and/or enumeration of bacteria,
 CC viruses and pathogens in food, beverages, water, pharmaceutical products,
 CC personal care products, dairy products, in clinical samples or in samples
 CC of plant, animal, human or environmental origin. They are also useful for
 CC the analysis of raw materials, equipment, products or processes used to
 CC manufacture or store food, beverages, water, pharmaceutical products,
 CC personal care products dairy products or environmental samples. The
 CC methods and materials are useful in areas such as expression analysis,
 CC SNP analysis, genetic analysis of humans, animals, fungi, yeast viruses
 CC and plants, therapy monitoring, pharmacogenomics, pharmacogenetics,
 CC epigenomics and high throughput screening operations. The present
 CC sequence is a PNA probe used for evaluation of combination oligomers.
 CC This sequence is used in the exemplification of the invention
 XX

Seq - Sequence 14 BP; 2 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 46.0%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 80;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTCGCTGCACGCA 19
 Db 14 CACGCTGACGTA 1

RESULT 55

AZ78944/c

ID AAZ78944 standard; DNA; 10 BP.

XX AAZ78944;

XX 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:1372.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 OS Homo sapiens.

XX WO9965924-A2.

XX

PD 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013800.
 PF 19-JUN-1998; 98US-0089833P.
 XX 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106077/09.
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX Claim 1; Page 104; 130pp; English.
 XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineages. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing

CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GGCACGCAC 20
 Db 9 GGCACGCAC 1
 RESULT 56
 AA278405
 ID AA278405 standard; DNA; 10 BP.
 XX AC AA278405;
 XX DT 10-APR-2000 (first entry)
 XX DE Human dendritic cell SAGE tag, SEQ ID NO:833.
 XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL; antitumor; ss.
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX OS Homo sapiens.
 XX PN WO9965924-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US013800.
 XX PR 19-JUN-1998; 98US-0089833P.
 XX PR 19-JUN-1998; 98US-0089844P.
 XX PR 19-JUN-1998; 98US-0089853P.
 XX PR 19-JUN-1998; 98US-0089878P.
 XX PR 19-JUN-1998; 98US-0089991P.
 XX PR 19-JUN-1998; 98US-0089992P.
 XX PR 19-JUN-1998; 98US-0089993P.
 XX PR 19-JUN-1998; 98US-0089994P.
 XX PR 19-JUN-1998; 98US-0089997P.
 XX PR 19-JUN-1998; 98US-0089999P.
 XX PR 19-JUN-1998; 98US-0090000P.
 XX PR 19-JUN-1998; 98US-0090035P.
 XX PR 19-JUN-1998; 98US-0090036P.
 XX PR 19-JUN-1998; 98US-0090039P.
 XX PR 19-JUN-1998; 98US-0090040P.
 XX PR 19-JUN-1998; 98US-0090041P.
 XX PR 19-JUN-1998; 98US-0090042P.
 XX PR 19-JUN-1998; 98US-0090043P.
 XX PR 19-JUN-1998; 98US-0090044P.
 XX PR 19-JUN-1998; 98US-0090045P.
 XX PR 19-JUN-1998; 98US-0090047P.
 XX PR 19-JUN-1998; 98US-0090048P.
 XX PR 19-JUN-1998; 98US-0090072P.
 XX PR 19-JUN-1998; 98US-0090076P.
 XX PR 19-JUN-1998; 98US-0090077P.
 XX PR 19-JUN-1998; 98US-0090078P.
 XX PR 19-JUN-1998; 98US-0090079P.
 XX PR 19-JUN-1998; 98US-0090080P.
 XX PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106077/09.
 XX
 DR Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 PT Claim 1; Page 89; 130pp; English.
 PS
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 XX expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGGCAGCGCA 19
 |||||
 Db 2 TGGCAGCGCA 10
 RESULT 57
 AAH64349
 ID AAH64349 standard; cDNA; 10 BP.
 XX
 AC AAH64349;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1189.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.
 XX
 XX 24-NOV-1999; 99US-0048480.
 XX
 XX (UVJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 XX
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 XX Claim 11; Page 66; 94pp; English.
 PS
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific. Cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGGCAGCGCA 19
 |||||
 Db 2 TGGCAGCGCA 10
 RESULT 58
 AAL45327/c
 ID AAL45327 standard; DNA; 10 BP.
 XX
 AC AAL45327;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human KCNB1 gene primer extension oligo SEQ ID NO: 41.
 XX
 KW Human; KCNB1; single nucleotide polymorphism; SNP; gene therapy;
 KW potassium voltage-gated channel; Shab-related subfamily, member 1;
 KW isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR;
 KW primer extension oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200204675-A1.
 XX
 PD 17-JAN-2002.
 XX
 XX 05-JUL-2001; 2001WO-US021307.
 XX
 XX 05-JUL-2000; 2000US-0215885P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Chew A, Choi JY, Koshiy B;
 PI WPI; 2002-188469/24.
 XX
 XX Isolated polymorphic variants of potassium voltage-gated channel, Shab-
 PT related subfamily, member 1 (KCNB1) gene useful for expressing KCNB1
 PT protein isoform to screen drugs to treat KCNB1 activity-related disease.
 XX
 XX Claim 18; Page 14; 180pp; English.

XX The present invention provides the protein, gene and cDNA sequences of
CC the human potassium voltage-gated channel, Shab-related subfamily, member
CC 1 (KCNB1) isogene and polymorphisms identified within these sequences.
CC The sequences can be used to screen drugs, which involves contacting the
CC polypeptide with a candidate agent, and to assay for binding activity as
CC a target for drugs to treat arrhythmia and seizures. The present sequence
CC is a primer extension oligonucleotide described in the invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GACTCGCTG 12
DB 10 GACTCGCTG 2
RESULT 59
ABL52050
ID ABL52050 standard; DNA; 10 BP.
XX
AC ABL52050;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:98.
XX
KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
KW haplotyping; genotyping; respiratory inflammatory disease;
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200222652-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US042217.
XX
PR 15-SEP-2000; 2000US-0232895P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Han J, Klieem SE, Sausker EA;
XX WPI; 2002-393942/42.
XX
PT Novel genetic variants of soluble carrier family 18 (vesicular
PT monoamine), member 2 gene useful for screening drugs to treat diseases
PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.
XX
PS Claim 19; Page 15; 183pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) having a
CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
CC sequence (S2) of 40023 bp (see ABL51954), and defined by a corresponding
CC set of polymorphisms whose locations and identities are given in the
CC specification; or a sequence (S2) complementary to (S1). (I) has
CC antiinflammatory and neuroleptic activities, and can be used in gene
CC therapy. Methods from the present invention can be used for haplotyping
CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying
CC the expression and function of SLC18A2, and in expressing the SLC18A2
CC protein for use in screening for candidate drugs to treat diseases
CC related to SLC18A2 activity and in studying the effect of the variation
CC on the biological activity of SLC18A2 as well as on the binding affinity
CC of candidate drugs targeting SLC18A2 for the treatment of respiratory

CC inflammatory diseases such as neuropsychiatric disorders involving
CC monoaminergic brain systems. The present sequence represents a preferred
CC oligonucleotide primer for human SLC18A2, which is given in the present
CC invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GCTGGCAGC 17
DB 2 GCTGGCAGC 10
RESULT 60
ABV63868
ID ABV63868 standard; cDNA; 11 BP.
XX
AC ABV63868;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1654.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 70; 1345pp; German.
XX
CC The invention relates to in vitro identification (MI) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression;
CC (MI) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GGCACGCAC 20
|||||

Db 3 GGCACGCAC 11

RESULT 61
ABV71289
ID ABV71289 standard; cDNA; 11 BP.
AC ABV71289;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9075.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 103; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
XX
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 12 GGCACGCAC 20
Db 3 GGCACGCAC 11
XX
RESULT 62
ABV65042
ID ABV65042 standard; cDNA; 11 BP.
XX
AC ABV65042;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2828.
XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 103; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10
XX
RESULT 63
AA34403
ID AA34403 standard; DNA; 12 BP.
XX
AC AA34403;
XX
DT 25-JUN-1999 (first entry)
XX
DE Template sequence Seq ID No: 3.
XX
KW Rolling template; nucleic acid synthesis; polynucleotide polymerase;
KW gene production; primer; ss.
XX
OS Synthetic.
XX
PN WO9914370-A1.
XX
PD 25-MAR-1999.
XX
PF 15-SEP-1998; 98WO-US019157.
XX
PR 15-SEP-1997; 97US-00929856.
XX

XX New asymmetric hammerhead ribozymes - used for cleaving target RNA for
PT treating e.g. viral or bacterial infection, neoplastic conditions or
PT psoriasis.
XX
XX Disclosure; Page 34; 49pp; English.
XX
XX New asymmetric hammerhead ribozymes have been developed, of the formula:
CC 5'-(N)n'NNN-C-U-G-A-[N-G-A-(N)m'-P-(N)m'-G-A-A-NNNNNN(N)n-3', where
CC N = a nucleotide which may be substituted or modified in its sugar, base
CC or phosphate provided not every N is a ribonucleotide; the hybridising
CC arms 3'-(N)NNNNNA and NNN (N)n-5' are each an oligonucleotide (ON)
CC having a predetermined sequence which is complementary to an RNA target
CC sequence to be cleaved; n and n' = an integer which defines the number of
CC nucleotides in the ON with the proviso that n = 1-5 and n' = 1 to 3; each
CC solid line represents chemical linkage providing covalent bonds between
CC the nucleotides located on either side; a = an integer which defines a
CC number of nucleotides with the proviso that a may be 0 or 1 and if 0, the
CC A located 5' of (N)a is bonded to the N located 3' of (N)a; in the stem-
CC loop of the compound each m and m' = an integer which is greater than 2;
CC P = a non-nucleotide linker or a nucleotide linker (N)b, where (N)b
CC represents an ON which may be present with the proviso that b = an
CC integer which is greater than or equal to 3. The present sequence
CC represents an oligonucleotide used in the present invention. The
CC ribozymes can be used for cleaving RNA target sequences. They can be used
CC for treating diseases (e.g. viral or bacterial infections, neoplastic
CC conditions, or psoriasis). They can also be used as diagnostics, e.g. to
CC detect a particular genetic defect or as RNA restriction enzymes or for
CC gene mapping
XX
XX Sequence 13 BP; 3 A; 5 C; 3 G; 1 T; 1 U; 0 Other;
SQ Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TGGACTCGC 10
Db 9 TGGACTCGC 1
RESULT 66
AAZ06013/C
ID AAA06013 standard; DNA; 13 BP.
XX
XX AAZ06013;
XX
XX 14-JUN-2000 (first entry)
XX
XX CFTR gene analysis oligonucleotide probe SEQ ID NO:23.
XX
XX CFTR; cystic fibrosis transmembrane conductance regulator; detection;
KW mutation; probe; human; hybridisation; ss.
XX
XX Homo sapiens.
XX
XX US6027880-A.
XX
XX 22-FEB-2000.
XX
XX 10-OCT-1995; 95US-00544381.
XX
XX 26-OCT-1993; 93US-00143312.
PR 02-AUG-1994; 94US-00284064.
PR 26-OCT-1994; 94WO-US012305.
PR 02-AUG-1995; 95US-00510521.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Huang XC, Chee M, Lobban PE, Hubbell EA, Sheldon EL, Miyada CG;
PI Cronin MT, Lipshutz RJ, Morris MS, Fodor SPA;
XX WPI; 2000-194825/17.
XX

XX An array of nucleic acid probes immobilized on a solid support, useful
PT for identifying mutations in the cystic fibrosis transmembrane
PT conductance regulator.
XX
XX Disclosure; Col 73; 114pp; English.
XX
XX The present invention describes an array of nucleic acid probes
CC immobilised on a solid support, which comprises: (1) a first probe set,
CC comprising probes with a segment of at least 6 nucleotides complementary
CC to the CFTR (cystic fibrosis transmembrane conductance regulator) gene,
CC where the segment includes at least 1 interrogation position
CC complementary to a nucleotide in the CFTR gene sequence; and (2) second,
CC third and fourth probe sets, each comprising probes identical to those in
CC (1) except that the interrogation position is occupied by a different
CC nucleotide. AAA05991 to AAA06240 represent CFTR gene analysis
CC oligonucleotide probes for use in the exemplification of the present
CC invention. The present invention also describes a method of comparing a
CC target nucleic acid with a reference sequence consisting of a
CC predetermined sequence of nucleotides, comprising: (a) hybridising a
CC sample comprising the target nucleic acid to an array of nucleic acid
CC probes immobilised on a solid support; (b) comparing the relative
CC specific binding of two corresponding probes from the first and second
CC probe sets; (c) assigning a nucleotide in the target sequence as the
CC complement of the interrogation position of the probe having the greater
CC specific binding; and (d) repeating (b) and (c) by comparing the relative
CC specific binding of a further two corresponding probes from the first and
CC second probe sets until each nucleotide of interest in the target
CC sequence has been assigned. The array is useful for analysis of the CFTR
CC gene, e.g. detection of mutations
XX
XX Sequence 13 BP; 0 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
SQ Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 GGCACGCAC 20
Db 11 GGCACGCAC 3
RESULT 67
AAZ40108/C
ID AAZ40108 standard; DNA; 13 BP.
XX
XX AAZ40108;
XX
XX 18-FEB-2000 (first entry)
XX
XX Detection probe #D203_1.
XX
XX Detection probe; electronic detection; conductive oligomer;
KW capture probe; nucleic acid detection; genetic diagnostic;
KW viral detection; bacterial detection; gene amplification detection;
KW DNA fingerprinting; ss.
XX
XX Synthetic.
XX
XX WO9957319-A1.
XX
XX 11-NOV-1999.
XX
XX 27-JAN-1999; 99WO-US001703.
XX
XX 06-MAY-1998; 98US-0084425P.
PR 06-MAY-1998; 98US-0084509P.
PR 17-AUG-1998; 98US-00135183.
XX
XX (CLIN-) CLINICAL MICRO SENSORS.
XX
XX Bamdad C, Yu C;
XX

DR WPI; 2000-038823/03.
 XX Components for the electronic detection of nucleic acids using conductive
 PT oligomers monolayers linked to probes.
 XX Example 7; Page 94; 164pp; English.
 XX This sequence represents a detection probe that can be used in the
 CC composition of the invention. The compositions comprise: (a) an electrode
 CC comprising: (i) a monolayer comprising conductive oligomers; and (ii) a
 CC capture probe; and either (b) a target sequence comprising a portion that
 CC can hybridize to the capture probe, and a second portion that does not
 CC hybridize to the probe and has at least 1 covalently attached electron
 CC transfer moiety (ETM); or (c) a label probe comprising a portion that can
 CC hybridize to a component of an assay complex and a second portion
 CC comprising a recruitment linker that does not hybridize to an assay
 CC complex component and has at least 1 covalently attached ETM. The probes
 CC are useful for the detection of a target nucleic acid sequences in
 CC samples, genetic diagnostics, viral or bacterial detection, forensic 'DNA
 CC fingerprinting', and for detecting successful gene amplification in PCR.
 CC The ETM's can be used as intermediates in the preparation of metalloene-
 CC backbone nucleic acid analogues
 XX
 SQ Sequence 13 BP; 3 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGACTCG 9
 Db 10 ATGGACTCG 2
 RESULT 68
 AAZ40248/c
 ID AAZ40248 standard; DNA; 13 BP.
 XX
 AC AAZ40248;
 DT 24-FEB-2000 (first entry)
 XX
 DE Detection probe #199_1.
 XX
 KW Detection probe; electronic detection; conductive oligomer; label probe;
 KW capture probe; nucleic acid detection; microorganism detection;
 KW genetic analysis; disease-associated gene detection; mutation detection;
 KW forensic fingerprinting; gene amplification detection;
 KW electron transfer molecule; ss.
 XX
 OS Synthetic.
 XX
 XX W09957317-A1.
 XX
 XX 11-NOV-1999.
 XX
 XX 06-MAY-1999; 99WO-US010104.
 XX
 XX 06-MAY-1998; 98US-0084509P.
 XX
 XX 06-MAY-1998; 98US-008452P.
 XX
 XX 17-AUG-1998; 98US-00135183.
 XX
 XX (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 XX Banded C, Yu C;
 XX
 XX WPI; 2000-052978/04.
 XX
 XX Electrode with a monolayer of conductive oligomers and insulators, with
 PT attached covalent capture ligand, used for, e.g. clinical or
 PT environmental assays.
 XX
 XX Example 8; Page 97; 143pp; English.

XX This sequence represents a detection probe that can be used in the
 CC composition of the invention. The composition comprises an electrode with
 CC a monolayer (A) consisting of conductive oligomers (I) and insulators,
 CC and a covalently attached capture binding ligand. The composition is
 CC used: (1) for environmental or clinical assays, for practically any
 CC analyte for which a ligand is available, e.g. pesticides, therapeutic or
 CC illicit drugs, hormones, immunoglobulins, nucleic acids, tumour or other
 CC cells, bacteria, viruses, antigens; (2) to screen for potential
 CC therapeutic agents (modulators of target/ligand interaction); (3) for
 CC genetic analysis, e.g. detecting disease-associated genes or mutations;
 CC (4) for forensic fingerprinting; and (5) to detect successful
 CC amplification in polymerase chain reactions. Electron transfer molecules
 CC (ETMs) can be detected directly on the surface of (A) containing (1). (A)
 CC shield the electrode from solution components and reduces the degree of
 CC non-specific binding. Many ETMs can be attached for increased
 CC sensitivity, e.g. 20-50 per recruitment linker
 XX
 SQ Sequence 13 BP; 3 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGACTCG 9
 Db 10 ATGGACTCG 2
 RESULT 69
 AAF30135/c
 ID AAF30135 standard; DNA; 13 BP.
 XX
 AC AAF30135;
 XX
 XX 30-APR-2001 (first entry)
 XX
 DE Positive control label probe.
 XX
 KW Probe; electron transfer moiety; ETM; detection; amplification;
 KW forensics; diagnosis; quality control; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT modified_base 2 /*tag= a
 FT /label= OTHER
 FT /note= "ETM attachment"
 FT modified_base 3
 FT /*tag= b
 FT /label= OTHER
 FT /note= "optional ETM attachment"
 XX
 XX W0200106016-A2.
 XX
 XX 25-JAN-2001.
 XX
 XX 20-JUL-2000; 2000WO-US019889.
 XX
 XX 20-JUL-1999; 99US-0144698P.
 XX
 XX (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 XX WPI; 2001-168467/17.
 XX
 XX Detection of a target nucleic acid for screening blood, water and food
 PT samples comprises using amplification techniques and an electron transfer
 PT moiety.
 XX
 XX Example 7; Page 123; 198pp; English.
 PS
 XX The present sequence represents a positive control label probe containing

CC 1 or 2 metal complexes as electron transfer moieties (ETMs). Experiments
 CC were performed to compare different ETM attachments. A detection probe
 CC was attached to an electrode surface, and positive (i.e. probes not
 CC complementary to the detection probe) and negative (i.e. probes not
 CC complementary to the detection probe) control labels were added. The
 CC electrodes were used in AC detection methods. The invention relates to
 CC methods useful in the detection of nucleic acids using a variety of
 CC amplification techniques, including both signal amplification and target
 CC amplification. Detection proceeds through the use of an ETM, preferably a
 CC metalloene and especially a ferrocene, that is associated with the
 CC nucleic acids, either directly or indirectly, to allow electronic
 CC detection of the ETM using an electrode. The extremely sensitive and
 CC specific probes can detect target sequences without removal of
 CC unhybridised probe, and are useful in a variety of forensic (e.g. DNA
 CC fingerprinting), research, clinical (e.g. genetic diagnosis), quality
 CC control or field testing settings

XX SQ Sequence 13 BP; 3 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGACTCG 9
 |||||
 Db 10 ATCGACTCG 2

RESULT 70

AAZ99838
 ID AAZ99838 standard; DNA; 12 BP.

XX AC AAZ99838;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of target oligonucleotide H.

XX KW Mono-length cDNA library; differential display; gene expression;
 XX KW gene identification; drug response; ss.

XX OS Synthetic.

XX PN WO200014273-A2.

XX PD 16-MAR-2000.

XX PF 26-AUG-1999; 99WO-CA000789.

XX PR 03-SEP-1998; 98US-00145936.

XX PA (SIGN-) SIGNALGENE INC.

XX PI Belouchi AM, Fournier H, Gee M, Gauvreau D;

XX DR WPI; 2000-257012/22.

XX PT Determining differential display of gene expression, useful for
 XX PT monitoring drug responses at the gene expression level and locating genes
 XX PT involved in a particular response, by comparisons between mono-length
 XX PT cRNA libraries.

XX PS Example 1; Page 43; 73pp; English.

XX CC AAZ99834-38 represent target oligonucleotides which were used to test for
 CC complementarity binding on three different types of membrane, in the
 CC course of the invention. The specification describes a method of
 CC determining differential display of gene expression, by comparison of
 CC mono-length cRNA libraries. These libraries are probe hybridised to
 CC accessible ordered arrays to determine differential hybridisation display
 CC sites between mono-length segment libraries and to locate genes of
 CC expression differential. The methods are useful for determining
 CC differential hybridisation display sites between mono-length segment

CC libraries and to locate genes of expression differential. The methods are
 CC also useful in gene identification related to complex traits. The methods
 CC also permit monitoring drug responses at the gene expression level and
 CC locating genes involved in a particular response. The methods are also
 CC useful for pharmacogenomic research in evaluating how variability in
 CC genetic background influences positive or negative response to a drug

XX SQ Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTGCC 14
 |||||
 Db 1 GGACTCGCTGCC 12

RESULT 71

AAZ99833/c
 ID AAZ99833 standard; DNA; 12 BP.

XX AC AAZ99833;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of probe oligonucleotide H.

XX KW Mono-length cDNA library; differential display; gene expression;
 XX KW gene identification; drug response; probe; ss.

XX OS Synthetic.

XX PN WO200014273-A2.

XX PD 16-MAR-2000.

XX PF 26-AUG-1999; 99WO-CA000789.

XX PR 03-SEP-1998; 98US-00145936.

XX PA (SIGN-) SIGNALGENE INC.

XX PI Belouchi AM, Fournier H, Gee M, Gauvreau D;

XX DR WPI; 2000-257012/22.

XX PT Determining differential display of gene expression, useful for
 XX PT monitoring drug responses at the gene expression level and locating genes
 XX PT involved in a particular response, by comparisons between mono-length
 XX PT cRNA libraries.

XX PS Example 1; Page 43; 73pp; English.

XX CC AAZ99826-33 represent probe oligonucleotides which were used to test for
 CC complementarity binding on three different types of membrane, in the
 CC course of the invention. The specification describes a method of
 CC determining differential display of gene expression, by comparison of
 CC mono-length cRNA libraries. These libraries are probe hybridised to
 CC accessible ordered arrays to determine differential hybridisation display
 CC sites between mono-length segment libraries and to locate genes of
 CC expression differential. The methods are useful for determining
 CC differential hybridisation display sites between mono-length segment
 CC libraries and to locate genes of expression differential. The methods are
 CC also useful in gene identification related to complex traits. The methods
 CC also permit monitoring drug responses at the gene expression level and
 CC locating genes involved in a particular response. The methods are also
 CC useful for pharmacogenomic research in evaluating how variability in
 CC genetic background influences positive or negative response to a drug

XX SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGTGGC 14
Db 12 GGACTCGTGGC 1

RESULT 72
ABH10648/C
ID ABH10648 standard; DNA; 12 BP.
XX AC ABH10648;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 310621 for detecting SNP TSC0024025.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 310621; 23pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 44.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 88;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGCGACGCAC 20
Db 12 GCGCGCACGCAC 1

RESULT 73
ABH86576
ID ABH86576 standard; DNA; 12 BP.
XX AC ABH86576;

XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286569 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 286569; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 2 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
XX Query Match 44.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 88;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GCGTGGCACGCA 19
Db 1 GCGCGCACGCA 12

RESULT 74
ABH86514/C
ID ABH86514 standard; DNA; 12 BP.
XX AC ABH86514;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286507 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.

PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 DR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 286507; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 44.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 CGCTGGCAGCGCA 19
 DB 12 CGCGCGCAGCGCA 1
 RESULT 75
 ABH86495/c
 ID ABH86495 standard; DNA; 12 BP.
 AC ABH86495;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 286488 for detecting SNP TSC0012735.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 286488; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 44.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 CGCTGGCAGCGCA 19
 DB 12 CGCGCGCAGCGCA 1
 RESULT 76
 ABH86557
 ID ABH86557 standard; DNA; 12 BP.
 AC ABH86557;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 286550 for detecting SNP TSC0012735.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 286550; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGCA 19
 ||| |||||
 Db 1 CGCAGCAGCA 12

RESULT 77

AB110641/c
 ID AB110641 standard; DNA; 12 BP.

XX
 AC AB110641;

XX
 DT 22-FEB-2002 (first entry)

XX
 DE Oligonucleotide primer SEQ ID NO 310614 for detecting SNP TSC0024025.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

XX
 PN WO200177384-A2.

XX
 PD 18-OCT-2001.

XX
 PF 06-APR-2001; 2001WO-IB000713.

XX
 PR 07-APR-2000; 2000DE-01019173.

XX
 PA (EPIG-) EPIGENOMICS AG.

XX
 PI Olek A, Piepenbrock C, Berlin K;

XX
 WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX
 PS Claim 1; SEQ ID NO 310614; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCAC 20

|| |||||

Db 12 GCACGCAGCAC 1

RESULT 78

ABC09578
 ID ABC09578 standard; DNA; 13 BP.

XX
 AC ABC09578;

XX
 DT 20-FEB-2002 (first entry)

XX
 DE Oligonucleotide SEQ ID NO 9569 for detecting SNP TSC0002510.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

XX
 PN WO200177384-A2.

XX
 PD 18-OCT-2001.

XX
 PF 06-APR-2001; 2001WO-IB000713.

XX
 PR 07-APR-2000; 2000DE-01019173.

XX
 PA (EPIG-) EPIGENOMICS AG.

XX
 PI Olek A, Piepenbrock C, Berlin K;

XX
 WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX
 PS Claim 1; SEQ ID NO 9569; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 13 BP; 1 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAATCGTGGC 14

||| |||||

Db 1 GGAATCGTGGC 12

RESULT 79

ABC09579/c
 ID ABC09579 standard; DNA; 13 BP.

XX
 AC ABC09579;

XX
 DT 20-FEB-2002 (first entry)

XX
 DE Oligonucleotide SEQ ID NO 9570 for detecting SNP TSC0002510.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 9570; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 44.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 3 GGACTCGCTGCGC 14
 DB 13 GGATTCGTGCGC 2
 RESULT 80
 ACD66039/c
 ID ACD66039 standard; RNA; 13 BP.
 XX AC ACD66039;
 XX DT 23-SEP-2003 (first entry)
 XX DE Anti-HCV nucleic acid molecule target sequence #62.
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNase; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; anti-HCV;
 KW viral replication; degenerative; disease state; HBV infection;
 KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
 KW hepatotropic; cytostatic; virucide; antiinflammatory; target; ss.
 XX Hepatitis C virus.
 OS WO200281494-A1.
 XX

PD 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX PR 26-MAR-2001; 2001US-00817879.
 XX PR 08-JUN-2001; 2001US-00877478.
 XX PR 08-JUN-2001; 2001US-0296876P.
 XX PR 24-OCT-2001; 2001US-0335059P.
 XX PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY J.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Claim 1; Page 319; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a target for one of the anti-
 CC HCV nucleic acid molecules disclosed in the present invention
 XX SQ Sequence 13 BP; 1 A; 2 C; 6 G; 0 T; 4 U; 0 Other;
 Query Match 44.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 ACTCGCTGCGAC 16
 DB 12 ACTCGCAAGCAC 1
 RESULT 81
 AAQ64030
 ID AAQ64030 standard; DNA; 10 BP.
 XX AC AAQ64030;
 XX DT 27-AUG-2003 (revised)
 XX DT 22-JUL-1994 (first entry)
 XX DE 16S rRNA gene fragment.
 XX 16S rRNA; probe; detection; procine atrophic rhinitis; hybridisation;
 KW Bordetella bronchiseptica; pig raising; ss.
 KW

XX OS Bordetella bronchiseptica.
XX XX JP05336999-A.
XX PD 21-DEC-1993.
XX PF 10-JUN-1992; 92JP-00150688.
XX PF 10-JUN-1992; 92JP-00150688.
XX (NISE-) NIHON SEIFUN KK.
XX (ZENK-) ZENKOKU NOGYO KD RENGOKAI.
XX WPI; 1994-037379/05.
XX B.bronchiseptica 16S rRNA fragments - used as probes in the detection of
PT porcine atrophic rhinitis.
XX XX Claim 1; Page 11; 12pp; Japanese.
XX DNA sequences (AAQ64009-Q64031) are fragments of the 16S rRNA gene from
CC B. bronchiseptica (AAQ5187). The fragments are used as probes to detect
CC porcine atrophic rhinitis caused by the Bordetella bronchiseptica
CC bacterium. Also claimed are 3 DNA fragments complementary to the 436-466
CC region of the 16S rRNA (AAQ64032-Q34). A specific DNA sequence from the S1
CC rRNA was selected and 2 probes were designed (AAQ64035 and AAQ64039) for
CC the detection of B.bronchiseptica. Primers (AAQ64036-37) were used to
CC clone the 16S gene. Sequences (AAQ64034) is the preferred probe used in
CC the detection process. (Updated on 27-AUG-2003 to correct OS field.)
XX XX Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGCATCGCT 11
Db 1 TGCATCGCT 10
RESULT 82
AAZ78956
ID AAZ78956 standard; DNA; 10 BP.
XX AC AAZ78956;
XX 10-APR-2000 (first entry)
XX Human dendritic cell SAGE tag, SEQ ID NO:1384.
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX Homo sapiens.
XX WO9965924-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013800.
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-0089991P.
XX 19-JUN-1998; 98US-0089992P.
XX 19-JUN-1998; 98US-0089993P.
XX 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B.L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX Claim 1; Page 104; 130pp; English.
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX them are used in gene therapy. Co-administration of tumour antigens and
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 9 GCTGGCAGGC 18
Db 1 GCTGGCAGGC 10

RESULT 83
AAZ77589
ID AAZ77589 standard; DNA; 10 BP.
AC
XX
XX
DT 10-APR-2000 (first entry)
DE Human dendritic cell SAGE tag, SEQ ID NO:17.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX
OS Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-0089919P.
XX 19-JUN-1998; 98US-0089992P.
XX 19-JUN-1998; 98US-0089993P.
XX 19-JUN-1998; 98US-0089994P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0089999P.
XX 19-JUN-1998; 98US-0090000P.
XX 19-JUN-1998; 98US-0090035P.
XX 19-JUN-1998; 98US-0090036P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX 19-JUN-1998; 98US-0090042P.
XX 19-JUN-1998; 98US-0090043P.
XX 19-JUN-1998; 98US-0090044P.
XX 19-JUN-1998; 98US-0090045P.
XX 19-JUN-1998; 98US-0090047P.
XX 19-JUN-1998; 98US-0090048P.
XX 19-JUN-1998; 98US-0090072P.
XX 19-JUN-1998; 98US-0090076P.
XX 19-JUN-1998; 98US-0090077P.
XX 19-JUN-1998; 98US-0090078P.
XX 19-JUN-1998; 98US-0090079P.
XX 19-JUN-1998; 98US-0090080P.
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 63; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene

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CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC, and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ

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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4 GACTCGCTGG 13
Db 1 GACCCGCTGG 10

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RESULT 84

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AAZ85891/c
ID AAZ85891 standard; DNA; 10 BP.

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XX AAZ85891;

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XX 07-APR-2000 (first entry)

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XX Metastatic breast tumour cell downregulated transcript tag #5125.

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XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

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XX Homo sapiens.

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XX WO9965928-A2.

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XX 23-DEC-1999.

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XX 18-JUN-1999; 99WO-US013647.

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XX 19-JUN-1998; 98US-0089853P.

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XX 19-JUN-1998; 98US-0089997P.

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XX 19-JUN-1998; 98US-0090039P.

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XX 19-JUN-1998; 98US-0090040P.

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XX (GENZ ) GENZYME CORP.

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XX (ROBE/) ROBERTS B L.

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PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 195; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TCGCTGGCAC 16
 Db 10 TCCCTGGCAC 1
 RESULT 85
 AAZ83491
 ID AAZ83491 standard; DNA; 10 BP.
 XX AAZ83491;
 AC AAZ83491;
 XX 07-APR-2000 (first entry)
 DT Metastatic breast tumour cell upregulated transcript tag #2725.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 XX 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.

PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 132; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 GCTGGCAGC 18
 Db 1 GCTGGCAGC 10
 RESULT 86
 AAZ85754/C
 ID AAZ85754 standard; DNA; 10 BP.
 XX AAZ85754;
 AC AAZ85754;
 XX 07-APR-2000 (first entry)
 DT Metastatic breast tumour cell downregulated transcript tag #4988.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 XX 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
DR
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 191; 219pp; English.
PS
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 CTGCGCAGCA 19
DB 10 CTGTCACGCA 1
RESULT 87
AAAS6201/c
ID AAAS6201 standard; DNA; 10 BP.
XX
XX AAAS6201;
XX
XX 07-SEP-2000 (first entry)
DT
XX Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:95.
DE
XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
XX Homo sapiens.
OS
XX WO200024892-A1.
PN
XX 04-MAY-2000.
PD
XX 28-OCT-1999; 99WO-JP005982.
PF
XX 28-OCT-1998; 98JP-00307532.
PR

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA Hashimoto S, Matsushima K, Suzuki T;
PI
XX WPI; 2000-350734/30.
DR
XX
XX Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
XX Claim 1; Page 58; 138pp; Japanese.
PS
XX The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAAS6107 to AAAS6386 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCAGCGCAC 20
DB 10 TGGCAGCGAAC 1
RESULT 88
AAZ79851
ID AAZ79851 standard; DNA; 10 BP.
XX
XX AAZ79851;
AC
XX 10-APR-2000 (first entry)
DT
XX Human dendritic cell preferentially expressed SAGE tag, SEQ ID NO:142.
DE
XX SAGE tag; serial analysis of gene expression; diagnosis;
KW differential gene expression; characterisation; targeted expression;
KW tumour; cancer; immunotherapy; ss.
XX
XX Homo sapiens.
OS
XX WO9666303-A2.
PN
XX 23-DEC-1999.
PD
XX 17-JUN-1999; 99WO-US013820.
PF
XX 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR

XX DR WPI; 2001-629566/73.

XX PT Human normal hepatocyte expression gene group.

XX PS Claim 1; Page 6; 26pp; Japanese.

XX CC The invention relates to a human normal hepatocyte expression gene group comprising 200 genes in the human normal hepatocyte. The cDNA of each gene comprises one of 200 fully defined nucleotide sequences as given in the specification. The gene group and the cDNAs corresponding to each of the genes in the group are useful in the diagnosis and treatment of human CC hepatopathy. The present sequence is a cDNA corresponding to a gene CC expressed by normal human hepatocytes

XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 95;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TGGACTCGCT 11

Db 1 TGGACGCGCT 10

RESULT 91

AAF41594

ID AAF41594 standard; DNA; 10 BP.

AC AAF41594;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8333.

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

XX Example; Page 297; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 95;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 CTCGCTGGCA 15

Db 1 CTGTCTGGCA 10

RESULT 92

ABV84757

ID ABV84757 standard; cDNA; 10 BP.

XX ABV84757;

XX 12-DEC-2002 (first entry)

XX Chronic hepatitis C/HCC differentially expressed gene SAGE tag #567.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.

XX Claim 46; Page 26; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX
 XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
 ||||| ||||
 Db 1 TGGACCCGCT 10

RESULT 93

ABV84542
 ID ABV84542 standard; cDNA; 10 BP.
 XX
 AC ABV84542;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human HCC underexpressed gene SAGE tag #352.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.

XX Claim 28; Page 20; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CARG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in

CC hepatocellular carcinoma compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
 ||||| ||||
 Db 1 TGGACCCGCT 10

RESULT 94

ABV84505
 ID ABV84505 standard; cDNA; 10 BP.

XX ABV84505;

XX 12-DEC-2002 (first entry)

XX Human apolipoprotein A-I SAGE tag #315.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.

XX Claim 28; Page 19; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CARG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with normal liver tissue

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
 |||||
 Db 1 TGGACGCGCT 10

RESULT 95

ABV84710
 ID ABV84710 standard; cDNA; 10 BP.

XX AC ABV84710;
 XX

DT 12-DEC-2002 (first entry)

DE Human apolipoprotein A-I SAGE tag #520.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

PF 19-JAN-2001; 2001JP-00012328.

PR 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.

XX Claim 46; Page 25; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
 |||||
 Db 1 TGGACGCGCT 10

RESULT 96

ABV84791
 ID ABV84791 standard; cDNA; 10 BP.

XX ABV84791;
 AC

DT 12-DEC-2002 (first entry)

XX Human apolipoprotein A-I SAGE tag #501.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.

XX Claim 55; Page 28; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
 CC expressed in chronic hepatitis C liver tissue
 XX

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
 |||||
 Db 1 TGGACGCGCT 10

RESULT 97

ABV84919
 ID ABV84919 standard; cDNA; 10 BP.

XX ABV84919;

XX 12-DEC-2002 (first entry)

XX Human apolipoprotein A-I SAGE tag #729.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;

XX PI Buckhaults P, Kinzler KW, Vogelstein B;
XX PD WPI; 2003-313220/30.
XX PF
XX PT Detecting colorectal cancer in a subject, involves detecting macrophage
XX PR inhibitory cytokine or renal dipeptidase or their mRNA in faeces or blood
XX PS of the subject.
XX PS Disclosure; Page 26; 59pp; English.
XX CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
XX CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
XX CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
XX CC amount of MIC or RDP detected to that in normal subjects, where an
XX CC elevated amount of MIC or RDP in the subject is an indicator of CC in
XX CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
XX CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
XX CC mRNA detected to that in normal subjects, where an elevated amount of MIC
XX CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
XX CC isolating epithelial cells from blood of a subject, isolating an mRNA
XX CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
XX CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
XX CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
XX CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
XX CC of CC in the subject; (d) contacting blood or faeces of a subject, with
XX CC an RDP substrate, detecting activity of RDP in the blood or faeces by
XX CC detection of increased reaction product or decreased RDP substrate, and
XX CC comparing the amount of activity of RDP in blood or faeces of the subject
XX CC to that in normal subjects, where an elevated amount of activity of RDP
XX CC in the blood or faeces of the subject is an indicator of CC in the
XX CC subject; (e) administering to a subject an antibody which specifically
XX CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
XX CC labeled with a moiety which is detectable from outside of the subject and
XX CC detecting the moiety in the subject from outside of the subject, where an
XX CC area of localisation of the moiety within the subject but outside the
XX CC proximal tubules of the kidney identifies CC; or (f) administering to a
XX CC subject a substrate for RDP, the substrate being labeled with a
XX CC detectable moiety, isolating faeces or blood from the subject, and
XX CC detecting in the faeces or blood RDP reaction product or decreased
XX CC with the detectable moiety, where increased product or decreased
XX CC substrate in the faeces or blood indicates CC in the subject. The methods
XX CC are useful for detecting colorectal cancer in a subject. The present
XX CC sequence is a DNA tag derived from a human transcript whose expression is
XX CC elevated in colorectal cancer or colorectal adenoma
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 TGGCAGCGAC 20
Db 10 TGGCAGCGAAC 1
RESULT 100
ACA94472/C
ID ACA94472 standard; DNA; 10 BP.
XX AC
XX AC ACA94472;
XX DT 18-JUL-2003 (first entry)
XX DE DNA tag from human transcript elevated in adenomas/cancers #53.
XX KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
XX KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
XX KW kidney proximal tubule.
XX OS Homo sapiens.
XX XX

PN WO2003022863-A1.
XX XX
XX PD 20-MAR-2003.
XX PF
XX PP 09-SEP-2002; 2002WO-US028518.
XX PR 07-SEP-2001; 2001US-0317494P.
XX PR 30-MAY-2002; 2002US-0383805P.
XX XX
XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX XX
XX PI Buckhaults P, Kinzler KW, Vogelstein B;
XX PD WPI; 2003-313220/30.
XX PF
XX PT Detecting colorectal cancer in a subject, involves detecting macrophage
XX PR inhibitory cytokine or renal dipeptidase or their mRNA in faeces or blood
XX PS of the subject.
XX PS Disclosure; Page 26; 59pp; English.
XX CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
XX CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
XX CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
XX CC amount of MIC or RDP detected to that in normal subjects, where an
XX CC elevated amount of MIC or RDP in the subject is an indicator of CC in
XX CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
XX CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
XX CC mRNA detected to that in normal subjects, where an elevated amount of MIC
XX CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
XX CC isolating epithelial cells from blood of a subject, isolating an mRNA
XX CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
XX CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
XX CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
XX CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
XX CC of CC in the subject; (d) contacting blood or faeces of a subject, with
XX CC an RDP substrate, detecting activity of RDP in the blood or faeces by
XX CC detection of increased reaction product or decreased RDP substrate, and
XX CC comparing the amount of activity of RDP in blood or faeces of the subject
XX CC to that in normal subjects, where an elevated amount of activity of RDP
XX CC in the blood or faeces of the subject is an indicator of CC in the
XX CC subject; (e) administering to a subject an antibody which specifically
XX CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
XX CC labeled with a moiety which is detectable from outside of the subject and
XX CC detecting the moiety in the subject from outside of the subject, where an
XX CC area of localisation of the moiety within the subject but outside the
XX CC proximal tubules of the kidney identifies CC; or (f) administering to a
XX CC subject a substrate for RDP, the substrate being labeled with a
XX CC detectable moiety, isolating faeces or blood from the subject, and
XX CC detecting in the faeces or blood RDP reaction product or decreased
XX CC with the detectable moiety, where increased product or decreased
XX CC substrate in the faeces or blood indicates CC in the subject. The methods
XX CC are useful for detecting colorectal cancer in a subject. The present
XX CC sequence is a DNA tag derived from a human transcript whose expression is
XX CC elevated in colorectal cancer or colorectal adenoma
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 TGGCAGCGAC 20
Db 10 TGGCAGCGAAC 1
RESULT 101
AAQ85812/C
ID AAQ85812 standard; DNA; 11 BP.
XX AC
XX AC AAQ85812;
XX XX

DT 25-MAR-2003 (revised)

XX 07-NOV-1995 (first entry)

DE 2'-O-alkylamino-containing oligomer #52.

XX Alkylamino group; ribofuranosyl sugar; antisense therapy; virus; HIV;

KW herpes; papilloma; antiviral; ss.

XX Synthetic.

OS

XX

FH Key Location/Qualifiers

FT modified_base 20

FT /tag= a

FT /mod_base= OTHER

FT /note= "optionally 5'-O-(dimethoxytrityl)-2'-O-(hexyl-

FT (omega-N-phthalimidoamino)-, 2'-O-hexyl-N-(1-pyrrene-

FT propyl-carbonyl)amino-, 2'-O-[6-bromoacetamido-hexyl]-,

FT or 2'-O-(hexyl-N-(polyethylene glycol)-propionyl)- amino

FT -uridine"

XX

XX W09506659-A1.

PN

XX

XX 09-MAR-1995.

PD

XX 02-SEP-1994; 94WO-US010131.

PF

XX 03-SEP-1993; 93US-00117363.

PR

XX (ISIS-) ISIS PHARM INC.

PA

XX Cook PD, Manoharan M, Guinosso CJ;

PI

XX WPI; 1995-115397/15.

DR

XX New amine-derivatised nucleoside(s) and oligo:nucleoside(s) - useful as

PT diagnostics, therapeutics and research reagents, partic. in anti-sense

PT therapy.

PT

XX Example 40; Page 52; 117pp; English.

PS

XX The sequence of an oligomer generated to contain a 2'-O-alkylamino-

CC modified nucleoside. The modified oligomer is an example of a compound

CC (see AAQ85799-Q85839 for other examples) e.g. a nucleoside or

CC oligonucleoside, which contains a ribofuranosyl sugar portion and a base

CC portion, such that at least one of the nucleoside contains at a 2'-O-, 3'

CC -O- or 5'-O-position, a substitution (see AAQ85799 for details of the

CC substitutions). The compounds are useful in diagnostics, therapeutics and

CC as research reagents particularly in antisense therapy for killing cells

CC and viruses such as HIV, herpes or papilloma viruses. (Updated on 25-MAR-

CC 2003 to correct PN field.)

XX

XX Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 1 Other;

SQ

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGCG 18

DB 11 CGCAGNCACGC 1

RESULT 102

ABQ86878

ID ABQ86878 standard; cDNA; 11 BP.

XX

XX ABQ86878;

AC

XX 10-SEP-2002 (first entry)

DT

XX Human skin stress/ageing related EST SEQ ID NO 633.

DE

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

KW

XX Homo sapiens.

XX W0200253773-A2.

PN

XX

XX 11-JUL-2002.

PD

XX 20-DEC-2001; 2001WO-BF015178.

PF

XX 03-JAN-2001; 2001DE-01000121.

PR

XX (HENK) HENKEL KGAA.

PA

XX Petersohn D, Conradt M, Hofmann K;

PI

XX WPI; 2002-528865/56.

DR

XX Identifying genes involved in skin stress and aging, useful e.g. in

PT screening for cosmetic or therapeutic agents, based on differential gene

PT expression.

PT

XX Claim 8; Page 63; 325pp; German.

PS

XX The invention relates to identifying (M1) genes in vitro that, in humans

CC or animals, are important for skin ageing and/or skin stress by serial

CC analysis of gene expression between mixtures of transcribed and

CC optionally translated, genetically encoded factors (A) obtained from

CC young and aged skin, to identify that genes that show strong differential

CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is

CC useful for: identifying markers of skin ageing and/or stress; determining

CC skin ageing and/or stress; and identifying or determining the effects of

CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed

CC sequence tags (ABQ86246-ABQ87680) of the invention

XX

SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCTGGCAGCG 18

DB 1 GCTGGCAGCG 10

RESULT 103

ABQ86592

ID ABQ86592 standard; cDNA; 11 BP.

XX

XX ABQ86592;

AC

XX 10-SEP-2002 (first entry)

DT

XX Human skin stress/ageing related EST SEQ ID NO 347.

DE

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

KW

XX Homo sapiens.

OS

XX W0200253773-A2.

PN

XX 11-JUL-2002.

PD

XX 20-DEC-2001; 2001WO-BF015178.

PF

XX 03-JAN-2001; 2001DE-01000121.

PR

XX (HENK) HENKEL KGAA.

PA

XX Petersohn D, Conradt M, Hofmann K;

PI

XX WPI; 2002-528865/56.

DR

XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.

XX Claim 8; Page 51; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention

XX Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

SQ Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCACCAC 20
Db 2 TGGCGCGCAC 11

RESULT 104
ABQ87015
ID ABQ87015 standard; cDNA; 11 BP.

XX AC ABQ87015;
XX 10-SEP-2002 (first entry)
XX Human skin stress/ageing related EST SEQ ID NO 770.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX Homo sapiens.
XX WO200253773-A2.
XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015178.
XX 03-JAN-2001; 2001DE-01000121.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.

XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.

XX Claim 8; Page 69; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention

XX Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGACTCGCTG 12
Db 2 GGACTCACTG 11

RESULT 105
ABQ86921/c
ID ABQ86921 standard; cDNA; 11 BP.

XX AC ABQ86921;
XX 10-SEP-2002 (first entry)
XX Human skin stress/ageing related EST SEQ ID NO 676.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX Homo sapiens.
XX WO200253773-A2.
XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015178.
XX 03-JAN-2001; 2001DE-01000121.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.

XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.

XX Claim 8; Page 65; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention

XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

SQ Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGC 14
Db 10 ACTGCTGGC 1

RESULT 106
ABQ87551

ID ABQ87551 standard; cDNA; 11 BP.
 AC ABQ87551;
 XX
 DT 10-SEP-2002 (first entry)
 DE Human skin stress/ageing related EST SEQ ID NO 1306.
 XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 KW Homo sapiens.
 XX
 OS WO200253773-A2.
 XX
 PN 11-JUL-2002.
 XX
 PD 20-DEC-2001; 2001WO-EP015178.
 XX
 PF 03-JAN-2001; 2001DE-01000121.
 XX
 PR (HENK) HENKEL KGAA.
 XX
 PA Petersohn D, Conradt M, Hofmann K;
 XX
 PI WPI; 2002-528865/56.
 XX
 DR Identifying genes involved in skin stress and aging, useful e.g. in
 XX screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 PT
 PT Claim 8; Page 91; 325pp; German.
 XX
 PS The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCGC 20
 |||||
 Db 2 TGGCAGCGC 11
 RESULT 107
 ABV63288
 ID ABV63288 standard; cDNA; 11 BP.
 XX
 AC ABV63288;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1074.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD In vitro identification of skin-expressed genes, useful for determining

PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 PF WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 54; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e-02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCGC 20
 |||||
 Db 2 TGGCAGCGC 11
 RESULT 108
 ABV71227
 ID ABV71227 standard; cDNA; 11 BP.
 XX
 AC ABV71227;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 9013.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 PF WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining

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PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 289; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 11 TGGCAGGCAC 20
 Db 2 TGGCAGGCAC 11
 |||||
 RESULT 109
 ABV70887
 ID ABV70887 standard; cDNA; 11 BP.
 AC
 AC ABV70887;
 DT 21-OCT-2002 (first entry)
 DE Human skin EST 8673.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.
 XX
 FN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 Claim 24; Page 278; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE).
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 11 TGGCAGGCAC 20
 Db 2 TGGCAGGCAC 11
 |||||
 RESULT 110
 ABV63627
 ID ABV63627 standard; cDNA; 11 BP.
 XX
 AC ABV63627;
 DT 21-OCT-2002 (first entry)
 DE Human skin EST 1413.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.
 XX
 FN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 Disclosure; Page 64; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 11 TGGCAGGCAC 20
 |||||

Db 2 TGGCAGGCAC 11

RESULT 111
ABV63806
ID ABV63806 standard; cDNA; 11 BP.
XX
AC ABV63806;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1592.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conzadt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PR Claim 24; Page 283; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (BST) of the invention
XX
PS Disclosure; Page 68; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (BST) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;
XX
OY 11 TGGCAGGCAC 20
| | | | | | | | | |
Db 2 TGGCAGGCAC 11
| | | | | | | | | |
RESULT 112
ABV71048
ID ABV71048 standard; cDNA; 11 BP.
XX
AC ABV71048;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8834.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conzadt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PR Claim 24; Page 283; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (BST) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;
XX
OY 11 TGGCAGGCAC 20
| | | | | | | | | |
Db 2 TGGCAGGCAC 11
| | | | | | | | | |
RESULT 113
ABV70709
ID ABV70709 standard; cDNA; 11 BP.
XX
AC ABV70709;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8493.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conzadt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PR Claim 24; Page 283; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (BST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;
XX
OY 11 TGGCAGGCAC 20
| | | | | | | | | |
Db 2 TGGCAGGCAC 11
| | | | | | | | | |
RESULT 113
ABV70709
ID ABV70709 standard; cDNA; 11 BP.
XX
AC ABV70709;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8493.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX

XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Claim 24; Page 271; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGGCAC 20
 |||||
 Db 2 TGGCAGGCAC 11
 RESULT 114
 ABV63167/c
 ID ABV63167 standard; cDNA; 11 BP.
 AC ABV63167;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 953.
 XX Human; skin; dermatological; vulvular; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 XX 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 51; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 ACTGGCTGGC 14
 |||||
 Db 10 ACTGGCTGGC 1
 RESULT 115
 ABV68745/c
 ID ABV68745 standard; cDNA; 11 BP.
 XX AC ABV68745;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 6531.
 XX Human; skin; dermatological; vulvular; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 XX 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 207; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX

SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGAC 20
 DB 10 TGGCAGCAAC 1

RESULT 116
 ABV69231
 ID ABV69231 standard; cDNA; 11 BP.
 AC ABV69231;
 XX
 XX
 XX 21-OCT-2002 (first entry)
 DT
 DE Human skin EST 7017.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.
 XX
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 DR
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PT
 XX Disclosure; Page 220; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 CC
 XX Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTG 12
 DB 2 GGACTCACTG 11

RESULT 117
 ABV63466
 ID ABV63466 standard; cDNA; 11 BP.
 AC ABV63466;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 DE Human skin EST 1252.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.
 XX
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 DR
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PT
 XX Disclosure; Page 59; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 CC
 XX Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGAC 20
 DB 2 TGGCAGCGAC 11

RESULT 118
 ABV70588/c
 ID ABV70588 standard; cDNA; 11 BP.
 AC ABV70588;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 DE Human skin EST 8374.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 117; 1345pp; German.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (SAGE) (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGCAC 20
Db 2 TGGCGGCGCAC 11
|||||
|||||

RESULT 120
ABV65566
ID ABV65566 standard; cDNA; 11 BP.
XX ABV65566;
AC ABV65566;
XX 21-OCT-2002 (first entry)
XX Human skin EST 3352.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
PA
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 118; 1345pp; German.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (SAGE) (MI) is useful for identifying genes involved in skin homeostasis; to

Query Match 42.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCTGG 13
 |||||
 Db 3 GACTCGCTGG 12

RESULT 123
 ACC58710
 ID ACC58710 standard; DNA; 12 BP.
 XX AC ACC58710;
 XX DT 26-AUG-2003 (first entry)
 XX DE Input molecule for molecular automaton.
 XX KW Computer; molecular automaton; ds.
 XX OS Synthetic.
 XX PN W02003042395-A2.
 XX PD 22-MAY-2003.
 XX PF 14-NOV-2002; 2002W0-IL000915.
 XX PR 14-NOV-2001; 2001US-03311318P.
 XX PR 07-JUN-2002; 2002US-0386418P.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX PI Shapero E, Benenson Y, Adar R, Paz-Elizur T;
 XX DR WPI; 2003-482351/45.
 XX PT Programmable finite biomolecular automaton for performing computation
 XX PR through manipulation of molecules, includes polymeric biomolecule, and
 XX PR biomolecule-manipulating components.
 XX PS Example 1; Fig 2; 52pp; English.
 XX CC The invention provides a device, system and method for a programmable
 CC finite automaton comprising a biomolecule, such as DNA, and associated
 CC biomolecule-manipulating enzymes, that solves computational problems
 CC autonomously. The hardware for the automaton preferably includes
 CC biomolecule-manipulating enzymes, such as restriction nucleases and
 CC ligases, the software and input are preferably encoded by double-stranded
 CC DNA, and programming is preferably performed by choosing appropriate
 CC software DNA molecules. The molecular computing machine uses the free-
 CC energy difference between its input and output to accomplish a
 CC computation, preferably using its input DNA molecule as a partial or the
 CC sole source of energy. It transforms an input DNA molecule into an output
 CC DNA molecule by digesting the input as it computes. An exemplary molecule
 CC finite automaton was implemented with a mixture of class IIS restriction
 CC nucleases FokI, T4 DNA ligase and ATP. The software comprised 8 short
 CC double-stranded (ds) transition molecules (see ACC58702-09), which encode
 CC the 8 possible transition rules. A dsDNA molecule, including the present
 CC sequence, encoded the initial state of the automaton and the input. The
 CC computation started when the hardware, software and input are mixed
 CC together and ran autonomously
 XX SQ Sequence 12 BP; 1 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCGCA 19
 |||||
 Db 1 CTGGCAGCGCA 10

RESULT 124
 AAA80866/c
 ID AAA80866 standard; DNA; 8 BP.
 XX AC AAA80866;
 XX DT 24-NOV-2000 (first entry)
 XX DE A. thaliana primer walking octamer SEQ ID NO: 179.
 XX KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
 XX OS Arabidopsis thaliana.
 XX PN US6083695-A.
 XX PD 04-JUL-2000.
 XX PF 21-MAY-1997; 97US-00859954.
 XX PR 15-APR-1996; 96US-00632782.
 XX PA (UYHO-) UNIV HOUSTON.
 XX PA (HARD/) HARDIN S H.
 XX PI Hardin PE, Hardin SH, Homayouni R;
 XX DR WPI; 2000-474852/41.
 XX PT Sequencing an unknown DNA molecule for the polymerase chain reaction and
 XX PR other primer processes comprises primer walking of octamer
 XX PR oligonucleotides.
 XX PS Example 8; Col 115-116; 161pp; English.
 XX CC This invention describes a novel method for sequencing an unknown DNA
 CC molecule which comprises selecting a library primer from an octamer
 CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
 CC complementary sequences, where the library primer is complementary to a
 CC known sequence adjacent to the unknown sequence or is complementary to a
 CC nucleotide sequencing, in PCR, and in other processes which make use of
 CC primers. The octamers are used to identify coding sequences. Primer
 CC walking using the octamer libraries is advantageous over other sequencing
 CC methods because it does not require multiple cloning steps nor subsequent
 CC template preparations, and it is a directed and methodical approach.
 CC AAA80868-A81253 represent the octamer primers used in the primer walking
 CC method of the invention
 XX SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
 |||||
 Db 8 ATGGACTC 1

RESULT 125
 AAL60738/c
 ID AAL60738 standard; DNA; 9 BP.
 XX AC AAL60738;
 XX DT 03-SEP-2003 (first entry)
 XX DE Human immune gene variable region amplifying TCRB 3' PCR primer.
 XX KW Human; immune gene repertoire; T-cell receptor; TCR; immune disorder;

therapy; immune gene; PCR; primer; ss.
 XX OS Homo sapiens.
 XX PN WO2003044225-A2.
 XX PD 30-MAY-2003.
 XX PF 15-NOV-2002; 2002WO-EP012822.
 XX PR 23-NOV-2001; 2001GB-00028153.
 XX PA (FARB) BAYER AG.
 XX PI Gehrman M, Schwes S, Weidler M;
 XX WPI; 2003-457620/43.
 XX DR Characterizing immune gene repertoire or detecting the presence of a
 XX PT specific immune gene in a vertebrate, comprises hybridizing the nucleic
 XX PT acid molecules representing the immune gene repertoire, to immobilized
 XX PT oligonucleotides.
 XX PS Claim 8; Fig 1; 42pp; English.
 XX CC The invention relates to a method for profiling immune gene repertoire or
 XX CC detecting the presence of a specific immune gene in a vertebrate. The
 XX CC method comprises hybridising the nucleic acid molecules representing the
 XX CC immune gene repertoire, to immobilised oligonucleotides. The method is
 XX CC useful for profiling the antibody and T-cell receptor (TCR) mRNA
 XX CC repertoire of an organism, and for detecting the presence of a specific
 XX CC immune gene in a vertebrate. Compounds that increase or reduce the
 XX CC transcription of at least one immune gene, the number of immune receptors
 XX CC and/or the number of immune cells in a vertebrate, are useful for
 XX CC treating an immune disorder. The present sequence is human immune gene
 XX CC variable region amplifying PCR primer consensus sequence. This sequence
 XX CC is used to illustrate the method of the invention
 XX SQ Sequence 9 BP; 1 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCTGGCAC 16
 Db |||||
 9 GCTGGCAC 2
 RESULT 126
 AAQ47917/c
 ID AAQ47917 standard; DNA; 10 BP.
 XX AC AAQ47917;
 XX DT 25-MAR-2003 (revised)
 XX DT 23-MAR-1994 (first entry)
 XX DE Primer for production of cDNA from mRNA.
 XX KW cDNA; mRNA; primer; PCR; polymerase chain reaction; poly A site; RT;
 XX KW reverse transcriptase; kozak sequence; ss.
 XX CS Synthetic.
 XX WO9318176-A1.
 XX PN 16-SEP-1993.
 XX PF 11-MAR-1993; 93WO-US002246.
 XX PR 11-MAR-1992; 92US-00850343.
 XX PR 11-MAR-1993; 93US-00033084.

XX (DAND) DANA FARBER CANCER INST INC.
 XX PI Liang P, Pardee AB;
 XX WPI; 1993-303488/38.
 XX DR Cloning and isolating mRNA as cDNA - by reverse transcription and
 XX PT polymerase amplification using two oligo-deoxy-nucleotide(s).
 XX PS Example 4; Page 17; 43pp; English.
 XX CC Two primers are used to amplify any given mRNA molecule in its cDNA form.
 XX CC The first primer is capable of binding either to (1) a site immediately
 XX CC upstream of the first adenine nucleotide of the poly A tail; (2) to a
 XX CC site including the mRNA's poly A signal sequence; (3) to a site including
 XX CC the mRNA's Kozak sequence or (4) to a sequence of an mRNA of which the
 XX CC nucleotide sequence is known. These primers are then extended by reverse
 XX CC transcriptase to produce the corresponding cDNA sequence. The second
 XX CC primer comprises an arbitrary sequence and is used alongside the first
 XX CC primer to amplify the cDNA molecule by PCR. This primer is a second
 XX CC arbitrary primer. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGCTGGC 14
 Db |||||
 9 TCGCTGGC 2
 RESULT 127
 AAQ99394/c
 ID AAQ99394 standard; DNA; 10 BP.
 XX AC AAQ99394;
 XX DT 12-FEB-1996 (first entry)
 XX DE Syngeneic and allogeneic transplant comparison primer, OPA-16.
 XX KW AIF-1; allograft inflammatory factor 1; transplant rejection; inhibitor;
 XX KW immunogenic; detection; diagnosis; ss.
 XX OS Synthetic.
 XX WO9517506-A1.
 XX PD 29-JUN-1995.
 XX PF 21-DEC-1994; 94WO-US014724.
 XX PR 21-DEC-1993; 93US-00171385.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Russell ME, Utans U;
 XX WPI; 1995-240668/31.
 XX PT DNA encoding allograft rejection factors and immunogenic fragments -
 XX PT useful for identifying transplant rejection inhibitors.
 XX PS Disclosure; Page 12; 138pp; English.
 XX CC AAQ99394-Q99396 are primers used to identify DNA from both allogeneic and
 XX CC syngeneic sources to determine where a specific gene is expressed. The
 XX CC AIF-1 gene is a differentially expressed allograft gene which is
 XX CC expressed in allograft tissue during transplant rejection. Identification
 XX CC of the AIF-1 product (AAR80520) or transcript indicates that allograft

CC rejection is taking place. The human AIF-1 gene and product are therefore useful in the diagnosis of transplant rejection. The diagnostic methods used allow rejection (vascular inflammation) to be detected at an early stage and require only a small amount of biopsy material

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 128
 AAT18616/c
 ID AAT18616 standard; DNA; 10 BP.

XX AAT18616;
 DT 06-NOV-1996 (first entry)
 DE Arbitrary 5' oligodecamer DDRT-PCR primer OPA 16.

XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
 KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
 KW rheumatoid arthritis; polymerase chain reaction; ss.

XX Synthetic.
 XX EP705842-A2.
 PN 10-APR-1996.

XX 02-OCT-1995; 95EP-00115510.
 XX 06-OCT-1994; 94EP-00115751.

XX (FARH) HOECHST AG.
 PI Bartnik E, Margerie D;
 XX WPI; 1996-181045/19.

XX Diagnosis and treatment of IL-1 mediated connective tissue diseases -
 PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
 PT antibodies to them.
 XX Example; Page 15; 31pp; English.

XX The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which
 CC were used along with 4 degenerate 3' oligo dT primers for the
 CC differential display of human chondrocyte mRNA by reverse transcription
 CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA
 CC clones, which were then searched against DNA databases for homology to
 CC known human genes. The cDNA mols. can be used for the prodn. of gene
 CC specific primers and probes to isolate genes induced by treating (esp.
 CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the
 CC diagnosis of IL-1beta related connective tissue diseases, in partic.
 CC osteoarthritis or rheumatoid arthritis

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 129
 AAT75144/c

ID AAT75144 standard; DNA; 10 BP.

XX AAT75144;

XX 04-MAR-1998 (first entry)

XX Arbitrary RT-PCR primer.

XX dhc-1; homocysteine, hypohomocysteinaemia; atherosclerosis; diagnosis;
 KW serum; Dam cell; PCR; arbitrary primer; messenger RNA pool; ss.

XX Synthetic.

XX WO9725440-A2.

XX 17-JUL-1997.

XX 02-JAN-1997; 97WO-CA000001.

XX 03-JAN-1996; 96US-00582261.

XX (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.

XX Austin RC, Hirsh J, Weitz J;

XX WPI; 1997-372877/34.

XX Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -
 PT and/or predisposition to develop premature atherosclerosis by detecting
 PT increased levels of serum homocysteine.

XX Disclosure; Page 22; 84pp; English.

XX Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from
 CC cells exposed to hyperphysiological, normal or subphysiological levels of
 CC homocysteine. PCR products were separated on a sequencing gel and
 CC discrete fractions which were increased or decreased were identified.
 CC This method was used to identify mRNA and the corresponding cDNA which
 CC are increased in the cells of a patient having hyperhomocysteinaemia or a
 CC predisposition to homocysteine mediated atherosclerosis. These
 CC polynucleotides can be used for the diagnosis and treatment of
 CC atherosclerotic diseases and diseases of metabolism of sulphur containing
 CC amino acids (e.g. homocysteinaemia), which are associated with vascular
 CC damage and atherosclerotic disease, specifically unstable angina, acute
 CC myocardial infarction (heart attack), cerebrovascular accidents (stroke),
 CC hypertension, renal artery stenosis, aortic stenosis and deep vein
 CC occlusive disease

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 130

AAV10688/c

ID AAV10688 standard; DNA; 10 BP.

XX AAV10688;

XX 21-JUL-1998 (first entry)

XX Human breast cancer gene differential display primer #6.

KW Breast cancer; malignant transformation; diagnostic; therapeutic;
 KW screening; primer; ss.

OS Synthetic.
 XX Homo sapiens.

XX WO9738085-A2.

XX 16-OCT-1997.

XX 09-APR-1997; 97WO-US005930.

XX 10-APR-1996; 96US-0015167P.

XX 05-JUN-1996; 96WO-US009286.

XX 06-JUN-1996; 96US-0019202P.

XX 11-JUL-1996; 96US-00678280.

XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX Smith H, Chen L;

XX WPI; 1997-512705/47.

XX Breast cancer genes - used to develop products to design or screen
 PT diagnostic reagents or therapeutic compounds.

XX Example 2; Page 46; 118pp; English.

CC Primers AAV10683-V10688 are used to obtain novel human breast cancer
 CC genes by differential display. The identified genes or fragments of these
 CC genes can be used for identifying genes and gene products that are
 CC intimately related to malignant transformation or maintenance of the
 CC malignant properties of cancer cells. It can also be used to design or
 CC screen diagnostic reagents or therapeutic compounds. Kits are included
 CC within the scope of the invention

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14

Db 9 TCGCTGGC 2

RESULT 131

AAV15590/c

ID AAV15590 standard; DNA; 10 BP.

XX AAV15590;

XX 02-JUL-1998 (first entry)

XX Human HPK-1A C4.8 and C21.7 PCR primer AP-1.

XX Cervical cancer; treatment; diagnosis; passage cell; lesion;

XX human foreskin keratinocyte cell line; HPK-1A; antibody; smear;

XX PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX DE19649207-C1.

XX 26-FEB-1998.

XX 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

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Duerst M, Nees M;

WPI; 1998-121623/12.

Nucleic acid characteristic of late or early passage cells immortalised
 by papilloma virus - and related polypeptide(s) and antibodies, used for
 diagnosis and treatment of cervical cancer and assessing potential for
 progression of cervical lesions.

Example 1; Page 4; 8pp; German.

PCR primers AAV15590 and AAV15591 are used to amplify fragments of the
 C4.8 and C21.7 genes from a human papillomavirus (HPV) immortalised human
 foreskin keratinocyte cell line HPK-1A. These genes are characteristic of
 late or early passage cells can be used in a method for assessing the
 potential for progression of cervical lesions. Antibodies generated
 against the encoded polypeptide are used for diagnosis of cervical cancer
 and to assess potential for lesion progression. Antibodies can also be
 used therapeutically by inhibiting the polypeptide. Antisense molecules
 based on the nucleotide sequence are used to inhibit expression of the
 protein. Detecting polypeptides, or related RNA, characteristic of late
 passage cells (which are potentially malignant) in cervical smears is a
 reliable way of assessing progression potential

Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14

Db 9 TCGCTGGC 2

RESULT 132

AAV50265/c

ID AAV50265 standard; DNA; 10 BP.

XX AAV50265;

XX 21-OCT-1998 (first entry)

Yeast tag for additional NORF chromosome 4 tag position 1324367.

Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
 eukaryotic cell; antifungal; SAGE tag; gene expression;
 serial analysis of gene expression; probe; ss.

Saccharomyces cerevisiae.

Synthetic.

WO9832847-A2.

30-JUL-1998.

22-JAN-1998; 98WO-US001216.

23-JAN-1997; 97US-0035917P.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Velulescu VE, Vogelstein B, Kinzler KW;

WPI; 1998-427943/36.

Yeast transcriptome - useful for modulating eukaryotic cell, for
 screening antifungal agents, and for identifying genes in cell cycle
 progression.

Claim 1; Page 26; 44pp; English.

CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
 CC involved in cell cycle progression selected from the group of
 CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
 CC tags for highly expressed genes and NORF genes are given in AAV50051 to
 CC AAV50345. The present invention describes: (1) a method of using yeast
 CC genes to modulate the cell cycle which comprises administering to a cell
 CC an isolated DNA molecule comprising a yeast gene which is involved in
 CC cell cycle progression selected from differentially expressed genes (SAGE
 CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
 CC antifungal drugs which comprises contacting a test substance with a yeast
 CC cell and monitoring expression of a yeast gene which is involved in cell
 CC cycle progression; (3) a method of identifying human genes which are
 CC involved in cell cycle progression which comprises hybridizing a probe
 CC comprising at least 10 contiguous nucleotides of a yeast gene which is
 CC differentially expressed between at least 2 phases selected from the log
 CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
 CC the phase in the cell cycle, where the probe comprises at least 14
 CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
 CC AAV50345), or as an array of probes on a solid support
 XX

SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
 |||||
 DB 10 GCACGCAC 3

RESULT 133
 AAX34945/C
 ID AAX34945 standard; DNA; 10 BP.

XX AAX34945;
 AC

XX 28-JUN-1999 (first entry)
 DT

DE PCR primer for DNA encoding a dehiscence zone protein ORS7(9).

XX Dehiscence zone protein; ORS7(9); regulation; pod dehiscence;
 KW

XX plant abscission; PCR primer; ss.
 XX

OS Synthetic.
 OS

XX Brassica napus.
 XX

XX WO9915680-A1.
 FN

XX 01-APR-1999.
 XX

XX 18-SEP-1998; 98WO-GB002836.
 PF

XX 19-SEP-1997; 97GB-00020038.
 PR

XX (BIOG-) BIOGENMA UK LTD.
 PA

XX Paul W, Roberts JA, Whitelaw C;
 PI

XX WPI; 1999-244427/20.
 DR

XX New Brassica napus nucleic acid and protein, useful for regulating pod
 PT dehiscence and/or plant abscission by producing transgenic plants or
 PT propagating material.
 PT

XX Example 1; Page 10; 20pp; English.
 PS

XX PCR primer AAX34944-45 were used to amplify DNA encoding a dehiscence
 CC zone protein designated ORS7(9). The ORS7(9) polynucleotides and
 CC polypeptides are useful for regulating pod dehiscence and plant
 CC abscission. Antisense ORS7(9) nucleic acid useful for preventing or
 CC reducing dehiscence or abscission
 CC

SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 DB 9 TCGCTGGC 2

RESULT 134

AAZ22961/C

ID AAZ22961 standard; DNA; 10 BP.

XX AAZ22961;
 AC

XX 10-JAN-2000 (first entry)
 DT

XX Arbitrary primer A.
 XX

XX Signal transduction protein; dehiscence; male sterile plant;
 KW shatter resistance; oilseed rape; primer; ss.
 XX

OS Synthetic.
 OS

XX WO9949046-A1.
 FN

XX 30-SEP-1999.
 PD

XX 22-MAR-1999; 99WO-GB000905.
 PF

XX 20-MAR-1998; 98GB-00006113.
 PR

XX (BIOG-) BIOGENMA UK LTD.
 XX

XX Wyatt P, Roberts JA, Whitelaw C;
 PI

XX WPI; 1999-580449/49.
 DR

XX A nucleic acid encoding a signal transduction protein involved in plant
 PT dehiscence, useful for producing shatter resistant male sterile plants.
 PT

XX Example 1; Page 23; 71pp; English.
 PS

XX The invention provides a nucleic acid encoding a signal transduction
 CC protein involved in the process of dehiscence. The nucleic acids and
 CC proteins are useful for regulating or controlling dehiscence of a pod or
 CC an anther in a plant, useful in the production of male sterile plants.
 CC The methods, etc. may be used in production of shatter resistance or
 CC shatter-delayed plants such as oilseed rape (Brassica napus)
 CC

SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 DB 9 TCGCTGGC 2

RESULT 135

AAZ26829/C

ID AAZ26829 standard; DNA; 10 BP.

XX AAZ26829;
 AC

XX 22-JUN-1999 (first entry)
 DT

XX PCR primer AP-1 used to amplify Rin2 cDNA sequences.
 DE

XX

KW Rin2; downregulation; functional response; allergy; asthma; hayfever;
 KW Ras-dependent signalling pathway; allergy; asthma; hayfever;
 KW atopic eczema; Ras-dependent cancer; neoplastic cellular proliferation;
 KW autoimmune disease; T cell-associated disease;
 KW T cell dependent graft vs. host disease; type I diabetes mellitus;
 KW multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis;
 KW wound healing; angiogenesis; re-epithelialization;
 KW human immune deficiency virus; immune suppression; cancer therapy;
 KW nerve regeneration; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9913079-A1.
 PN
 PD 18-MAR-1999.
 XX
 XX PF 11-SEP-1998; 98WO-US019056.
 XX
 PR 11-SEP-1997; 97US-0058520P.
 PR 02-OCT-1997; 97US-00942819.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Tam S, Tsai M, Galli SJ;
 XX
 DR WPI; 1999-229239/19.
 XX
 XX Rin2 polypeptides and related nucleic acid.
 PT
 XX
 PS Disclosure; Page 47; 101pp; English.
 XX
 CC The present sequence represents a primer used to amplify Rin2 cDNA
 CC sequences. Rin2 polypeptides downregulate functional responses elicited
 CC by Ras-dependent signalling pathways. Agents that increase Rin2 activity
 CC (particularly Rin2 itself, optionally expressed from a vector) are used
 CC to treat allergy (asthma, hayfever or atopic eczema); Ras-dependent
 CC cancers and (non-)neoplastic cellular proliferation; autoimmune diseases;
 CC T cell-associated diseases and T cell dependent graft vs. host disease
 CC (typical examples being type I diabetes mellitus; multiple sclerosis;
 CC Crohn's disease, autoimmune hepatitis and psoriasis). Agents that inhibit
 CC Rin2 activity are used to improve wound healing; angiogenesis and/or re-
 CC epithelialization (also to improve immune response to pathogens; in human
 CC immune deficiency virus, and some other, infections; immune suppression
 CC associated with cancer therapy, and nerve regeneration)
 XX
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 TCGCTGCG 14
 DB 9 TCGCTGCG 2
 RESULT 136
 AA225357/c
 ID AA225357 standard; DNA; 10 BP.
 XX
 AC AA225357;
 XX
 DT 17-DEC-1999 (first entry)
 XX
 DE Rat DRN PCR primer #1.
 XX
 KW DRN; secreted protein; cell growth inhibition; fusion protein; tumour;
 KW green fluorescent protein; GFP; hyperproliferative cell disorder; ss.
 KW enhanced green fluorescent protein; EGFP; diagnosis; PCR primer; ss.
 XX
 OS Synthetic.
 OS Rattus sp.
 XX

PN WO9949041-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 26-MAR-1999; 99WO-US006675.
 XX
 PR 26-MAR-1998; 98US-0079440P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Blair DG, Clausen PA, Topol LZ, Marx M, Calothy G;
 XX
 DR WPI; 1999-591095/50.
 XX
 PD New isolated nucleic acid encoding DRM protein, for regulation of cell
 PT growth, particularly treating cancer and.
 XX
 XX Example 1; Page 31; 115pp; English.
 PS
 CC The present invention describes nucleic acids comprising human, murine or
 CC rat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos
 CC -transformed cells, drn gene). The nucleic acids, and DRM proteins, are
 CC useful for arresting cell growth; inhibiting tumour cell growth; treating
 CC hyperproliferative cellular disorders, either in vivo or ex vivo and
 CC producing fusion proteins with enhanced green fluorescent protein (EGFP)
 CC of increased stability (useful in screening assays, protein- protein
 CC interaction studies, cell labeling and as markers during purification).
 CC Detecting abnormally low levels of DRM, or the nucleic acids, may be used
 CC to identify subjects with an increased risk of developing a
 CC hyperproliferative disease. Fragments of the nucleic acids are useful as
 CC probes and primers to detect or quantify drn and to screen genomic and
 CC cDNA libraries. Antibodies raised against DRM can be used to
 CC detect/quantify DRM in immunoassays. Fusion proteins of DRM and GFP are
 CC localised to the nucleus (in contrast cytoplasmic localisation of GFP
 CC itself) and so are more stable, e.g. on exposure to fixatives or
 CC detergents, and thus form more versatile reagents, e.g. they can be used
 CC in fluorescence-based assays that require cell fixation, or linked to
 CC proteins or antibodies for use in enzyme-linked immunosorbent assays.
 CC Stable EGFP can be attached to proteins during synthesis, allowing the
 CC labeling of materials that are too unstable for chemical modification.
 CC The present sequence represents a PCR primer for rat DRM
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 TCGCTGCG 14
 DB 9 TCGCTGCG 2
 RESULT 137
 AA299304/c
 ID AA299304 standard; DNA; 10 BP.
 XX
 AC AA299304;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Probe used to obtain cancer associated gene cDNA sequences.
 XX
 KW Cancer associated gene; cancer specific gene; C1-9a11-2; CH8-2a13-1;
 KW CH13-2a12-1; CH14-2a16-1; cancer; gene duplication; RNA overabundance;
 KW breast cancer; lung cancer; glioblastoma; pancreatic cancer;
 KW colon cancer; prostate cancer; hepatoma; myeloma; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009655-A2.
 XX
 XX 24-FEB-2000.
 PD

XX 10-AUG-1999; 99WO-US018101.
 XX 10-AUG-1998; 98US-00132029.
 XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
 XX (USGO) US GOVERNMENT.
 XX Chen L;
 XX WPI; 2000-224318/19.
 XX New cancer associated polypeptides, genes encoding them and antibodies
 XX against them, useful for diagnosing breast cancer and screening for
 XX anticancer drugs.
 XX Example 2; Page 87; 154pp; English.
 XX
 XX AAZ9299-299304 represent probes used to isolate cancer associated gene
 XX cDNA sequences. These cancer specific genes are designated CI-9a11-2, CH8
 XX -2a13-1, CH13-2a12-1, and CH14-2a16-1. These genes show RNA overabundance
 XX in a majority of cancer cell lines tested, as well as a gene duplication
 XX in many of the cancers. Probes and primers derived from the
 XX polynucleotide sequence may be used to measure or detect altered gene
 XX duplication or overabundance of RNA in cancerous cells. This allows the
 XX screening of cancer, especially breast cancer, by correlating gene
 XX duplication of RNA overexpression obtained in this method with an
 XX increased risk for cancer. The polypeptide, and its antibodies, are used
 XX as reagents for detecting altered protein expression in cancerous cells.
 XX Both the cancer associated polypeptide and polynucleotide may be used to
 XX screen for candidate drugs for cancer treatment. They are also used in
 XX gene therapy to treat cancers such as lung cancer, glioblastoma,
 XX pancreatic cancer, colon cancer, prostate cancer, hepatoma, myeloma and
 XX breast cancer
 XX
 XX Query Match 40.0%; Score 8; DB 1; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGGTGGC 14
 DB 9 TCGGTGGC 2
 RESULT 138
 ID AAZ78859/c
 XX AAZ78859 standard; DNA; 10 BP.
 AC AAZ78859;
 XX
 XX 10-APR-2000 (first entry)
 DE Human dendritic cell SAGE tag, SEQ ID NO:1287.
 XX
 XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO9965924-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013800.
 XX
 XX 19-JUN-1998; 98US-0089833P.
 XX 19-JUN-1998; 98US-0089844P.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 08-DEC-1998; 98US-011715P.
 XX
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 102; 130pp; English.
 XX
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 XX expression) tags used to identify mRNA transcripts encoding or
 XX immunostimulatory cofactor proteins which are preferentially or
 XX differentially expressed in monocyte-derived dendritic cells compared
 XX with monocytes. Some of the transcripts correspond to known genes or ESTs
 XX (expressed sequence tags) which were previously unknown to be
 XX preferentially or differentially expressed in dendritic cells, while
 XX other transcripts correspond to novel genes. Antigen-presenting cell
 XX (APC)-associated costimulatory factors play an important role in the
 XX activation of the cytotoxic immune response, particularly against tumour
 XX cells. Tumour antigen presentation via the MHC (major histocompatibility
 XX complex) and subsequent recognition by T-cell receptors is alone
 XX insufficient to activate a robust cytotoxic immune response that can lyse
 XX the tumour cells. Immunostimulatory cofactors also being required for
 XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 XX sequences identified using the SAGE tags have several potential uses.
 XX They may be used in vaccines to induce an immune response, particularly
 XX against a tumour antigen; to modulate the genotype of an APC; to screen
 XX for agents that modulate expression of differentially expressed genes in
 XX an APC; and as hybridisation probes/amplification primers for the
 XX diagnosis, prognosis and monitoring of diseases related to abnormal
 XX expression of these genes. Detection of the dendritic cell differentially
 XX expressed genes, or of their encoded proteins, can be used to identify
 XX cells as belonging to the monocyte lineage. Cells containing these genes
 XX can be used in active immunotherapy (or to stimulate production of a
 XX population of antigen-specific effector cells) and vectors containing
 XX them are used in gene therapy. Co-administration of tumour antigens and
 XX APC-associated costimulatory factors ensures adequate antigen
 XX presentation to endogenous APCs and upregulates the APCs for the
 XX presentation of co-stimulatory signals, migration to T cell-rich sites,
 XX recruitment of T cell growth factors and secretion of chemokines for
 XX recruitment of immune effector cells
 XX
 XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTGC 9
 DB 10 TGGACTGC 3

RESULT 139

AAZ79496
 ID AAZ79496 standard; DNA; 10 BP.

XX AAZ79496;

XX 10-APR-2000 (first entry)

DT Human dendritic cell SAGE tag, SEQ ID NO:1924.

DE SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089911P.

PR 19-JUN-1998; 98US-0089922P.

PR 19-JUN-1998; 98US-0089933P.

PR 19-JUN-1998; 98US-0089944P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.

PR 19-JUN-1998; 98US-0090078P.

PR 19-JUN-1998; 98US-0090079P.

PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.

PA (ROBE) ROBERTS B. L.

PA (SHAN) SHANKARA S.

XX Roberts BL, Shankara S;

DR WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 119; 130pp; English.
 PS Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
 XX expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGGC 18
 DB 2 TGGCAGGC 9

RESULT 140

AAZ50856/c

ID AAZ50856 standard; DNA; 10 BP.

XX AAZ50856;

AC AAZ50856;

DT 31-MAY-2000 (first entry)

DE Primer API to identify tobacco salicylic acid inducible genes.

XX Tobacco plant; salicylic acid inducible gene; fungal pathogen;

KW SA-inducible gene; transgenic plant; pathogen resistance; PCR primer; ss.

XX Nicotiana tabacum.

OS WO2000008186-A1.

PN 17-FEB-2000.

PD 02-AUG-1999; 99WO-EP005581.

XX 03-AUG-1998; 98US-00895187P.

XX (MOGE-) MOGEN INT NV.

XX Stuiver MH, Jepson I, Horvath DM, Chua N;

XX WPI; 2000-205725/18.
 XX Novel salicylic acid inducible genes from tobacco plants, useful for
 PT making transgenic plants with enhanced pathogenic resistance.
 XX Example 1; Page 51; 57pp; English.
 CC The patent discloses fifteen new salicylic acid (SA) inducible genes from
 CC Nicotiana tabacum, nine of which were subcloned and sequenced. Based on
 CC different kinetics of induction response, these genes were classified
 CC into four categories, class I, II, III and IV response genes. The SA-
 CC inducible genes are useful for making transgenic plants with enhanced
 CC pathogen resistance. The plants incorporating these genes show reduced
 CC susceptibility to fungal pathogens. The present sequence is an upstream
 CC primer API used in differential display PCR reactions along with
 CC downstream primers T12MG or T12MC to identify tobacco SA-inducible genes
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGCTGCG 14
 Db 9 TCGCTGCG 2
 RESULT 141
 AAZ83127
 ID AAZ83127 standard; DNA; 10 BP.
 AC AAZ83127;
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell upregulated transcript tag #2361.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 PF 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 PI Roberts BL, Shankara S;
 DR WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 122; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 Db 2 GCACGCAC 9
 RESULT 142
 AAZ84391
 ID AAZ84391 standard; DNA; 10 BP.
 AC AAZ84391;
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #3625.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 PF 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 PI Roberts BL, Shankara S;
 DR WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 155; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGCG 18

Db 2 TGGCAGCG 9

RESULT 143

AAZ81505/c
 ID AAZ81505 standard; DNA; 10 BP.

AC AAZ81505;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #739.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW anti-metastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

PS Claim 1; Page 78; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCA 19

Db 10 GGCACGCA 3

RESULT 144

AAZ82875/c
 ID AAZ82875 standard; DNA; 10 BP.

AC AAZ82875;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #2109.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW anti-metastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

PT treatment of cancer.
 XX
 PS
 XX Claim 1; Page 116; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines, for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGACTC 8
 Db 10 ATGGACTC 3
 RESULT 145
 AAZ84842/c
 ID AAZ84842 standard; DNA; 10 BP.
 XX
 AC AAZ84842;
 XX
 XX 07-APR-2000 (first entry)
 DT
 XX Metastatic breast tumour cell downregulated transcript tag #4076.
 DE
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965928-A2.
 PN
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR
 XX 19-JUN-1998; 98US-0089997P.
 PR
 XX 19-JUN-1998; 98US-0080039P.
 PR
 XX 19-JUN-1998; 98US-0090040P.
 PR
 XX 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 DR WPI; 2000-106079/09.
 XX

PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS
 XX Claim 1; Page 167; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines, for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CTGGCAOG 17
 Db 10 CTGGCAOG 3
 RESULT 146
 AAZ84408/c
 ID AAZ84408 standard; DNA; 10 BP.
 XX
 AC AAZ84408;
 XX
 XX 07-APR-2000 (first entry)
 DT
 XX Metastatic breast tumour cell downregulated transcript tag #3642.
 DE
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965928-A2.
 PN
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR
 XX 19-JUN-1998; 98US-0089997P.
 PR
 XX 19-JUN-1998; 98US-0090039P.
 PR
 XX 19-JUN-1998; 98US-0090040P.
 PR
 XX 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 DR
 XX

DR WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 156; 219pp; English.
 PS
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCTGGCAC 16
 Db 8 GCTGGCAC 1
 |||||
 |||||
 RESULT 147
 AAZ82943
 ID AAZ82943 standard; DNA; 10 BP.
 AC AAZ82943;
 XX
 XX 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell upregulated transcript tag #2177.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE//) ROBERTS B L.
 PA (SHAN//) SHANKARA S.
 XX

PI Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 118; 219pp; English.
 PS
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGACTCG 9
 |||||
 |||||
 Db 3 TGGACTCG 10
 RESULT 148
 AAZ84948/C
 ID AAZ84948 standard; DNA; 10 BP.
 AC AAZ84948;
 XX
 XX 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #4192.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE//) ROBERTS B L.
 PA

PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 170; 219pp; English.
 XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 XX Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CGCTGGCA 15
 |||||
 DB 8 CGCTGGCA 1
 RESULT 149
 AA14157/c
 ID AA14157 standard; DNA; 10 BP.
 XX AA14157;
 AC
 XX 15-SEP-2003 (revised)
 DT 21-JUL-2000 (first entry)
 XX
 DE E. coli K-12 lagging strand PCR primer, SEQ ID NO:55.
 XX
 KW Polymorphism detection; over-represented sequence; strand bias;
 KW organism identification; genomic mapping; octamer; lagging strand;
 KW Escherichia coli 0157:H7; PCR primer; ss.
 XX
 OS Escherichia coli K12.
 XX
 XX WO200017399-A2.
 FN
 XX 30-MAR-2000.
 PD
 XX 17-SEP-1999; 99WO-US021379.
 PF
 XX 18-SEP-1998; 98US-0101011P.
 PR
 XX (UYNE-) UNIV NEBRASKA-LINCOLN.
 PA
 XX Benson AK;
 PI

XX WPI; 2000-283618/24.
 DR Detecting DNA polymorphisms, useful e.g. for identifying organisms by
 XX species, strain or serotype, comprises amplification with primers based
 PT on over-represented oligonucleotide sequences.
 XX Example; Page 28; 49pp; English.
 PS
 XX The invention relates to a novel method for the detection of
 CC polymorphisms in a DNA sequence. Test DNA and a second DNA are amplified
 CC with at least one pair of primers, and the sequence differences between
 CC the amplicons are compared. The primers are based on oligonucleotide
 CC sequences that are over-represented in the genome of the relevant
 CC organism, and which are biased to one strand. The method can be used to
 CC identify an organism by species, serotype or strain, in which case
 CC amplicons are analysed for products common to all members of the
 CC species, and those specific for strain or serotype, and the results
 CC compared with an existing database. The method can also be used to
 CC identify an individual, by comparison of results for a test DNA with an
 CC existing database. When applied to differential display analysis, pattern
 CC differences in the amplicons are determined, particularly by a
 CC quantitative method such as densitometry, fluorimetry or radiometry. The
 CC method of the invention is used to identify individuals, to classify
 CC organisms by species, strain or serotype, and to identify genes based on
 CC differential display. The method can also be used for genomic mapping,
 CC detecting changes in expression patterns, genetic linkage studies,
 CC medical diagnosis, epidemiology, forensics, and agriculture. The method
 CC uses over-represented sequences to prime amplification. These sequences
 CC are distributed over the entire genome, so analysis is not restricted to
 CC particular regions, and a single primer pair can amplify up to 5% of the
 CC complete Escherichia coli genome. The primers are rationally designed, so
 CC non-specific amplification is limited and the method does not require
 CC restriction enzymes or adapters. Sequences AA14155-AA14160 represent PCR
 CC primers based on over-represented octamer sequences biased to the lagging
 CC strand of the E. coli K-12 genome. These primers, and leading strand
 CC primers AA14149-AA14154 were used in the exemplifications of the
 CC invention to differentiate and further characterise two strains of E.
 CC coli 0157:H7 (strains FR1641 and FR1K 533) and two strains from the
 CC ECOR collection (ECOR 20 and ECOR 50). (Updated on 15-SEP-2003 to
 CC standardise OS field)
 XX
 XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CGCTGGCA 15
 |||||
 DB 9 CGCTGGCA 2
 RESULT 150
 AA248447/c
 ID AA248447 standard; DNA; 10 BP.
 XX AA248447;
 AC
 XX 27-MAR-2000 (first entry)
 DT
 XX
 XX Primer specific for C. jejuni.
 DE
 XX Microorganism; virus; polymerase chain reaction; food; cosmetic;
 KW clinical diagnostic; molecular beacon; PCR primer; ss.
 KW Campylobacter jejuni.
 OS
 XX WO963112-A2.
 PN
 XX 09-DEC-1999.
 PD
 XX 18-MAY-1999; 99WO-US010940.
 PF

XX 18-MAY-1998; 98US-0085025P.
 PR 17-MAY-1999; 99US-00086025.
 XX
 XX (HUNT-) HUNT WESSON INC.
 XX PA
 XX Romick TL, Fraser MS;
 XX PI
 XX WPI; 2000-086985/07.
 XX DR
 XX
 XX Detection of microorganisms and viruses, for use in the food and cosmetic
 PT industries and for clinical diagnostics.
 XX PT
 XX Disclosure; Page 25; 63pp; English.
 XX PS
 XX The invention provides a novel in vitro method for the detection of
 CC microorganisms and viruses. The method comprises: (1) forming a
 CC polymerase chain reaction (PCR) mixture by combining a predetermined
 CC volume of a sample to be tested for the presence of a nucleic acid
 CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
 CC comprising 5'-GCTAAGGTCCCAAGT-3', and a second primer comprising 5'-
 CC AGAAGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by
 CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
 CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)
 CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTCTAAGCCAC-3' to
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
 CC the nucleic acid sequence, if present, and change the conformation of the
 CC probe; and (4) determining whether or not bacteria are present in the
 CC sample by detecting the conformational change of the probe, a
 CC conformational change indicating the presence of bacteria in the sample.
 CC The methods can be used for the detection of viruses and microorganisms,
 CC including bacteria, yeast, molds and protozoa. They can be used in the
 CC food and cosmetic industry and in clinical diagnostics. Using the method
 CC it is not necessary to remove non-hybridized probe from the system
 XX
 XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGCTGGC 14
 Db 9 TCGCTGGC 2
 RESULT 151
 AAA65614/C
 ID AAA65614 standard; DNA; 10 BP.
 XX AC
 XX AAA65614;
 XX DT
 XX 14-NOV-2000 (first entry)
 XX DE
 XX Allograft inflammatory factor related PCR primer SEQ ID NO:28.
 XX KW
 XX Allograft inflammatory factor 1; AIF-1; AIF-2; allograft gene; screening;
 KW diagnosis; allograft rejection; vascular inflammation; atherosclerosis;
 KW immunosuppressive; antiinflammatory; antiarteriosclerotic; PCR primer;
 KW ss.
 XX OS
 XX Rattus sp.
 XX PN
 XX US6077948-A.
 XX PD
 XX 20-JUN-2000.
 XX PF
 XX 21-DEC-1994; 94US-00361441.
 XX PR
 XX 21-DEC-1993; 93US-00171385.
 XX PA
 XX (HARD) HARVARD COLLEGE.

PI Utans U, Russell ME;
 XX DR
 XX WPI; 2000-430614/37.
 XX PT
 XX DNA encoding an allograft inflammatory factor-1, useful for diagnosing
 PT and treating allograft rejection and other conditions associated with
 PT vascular inflammation, especially atherosclerosis.
 XX PT
 XX Example 1; Col 6; 59pp; English.
 XX PS
 XX The present invention describes isolated DNA (I) encoding an allograft
 CC inflammatory factor-1 (AIF-1). AIF-1 has immunosuppressive,
 CC antiinflammatory and antiarteriosclerotic activities. AIF-1 is an
 CC inhibitor of expression of allograft factor such as Gal/GalNAc macrophage
 CC lectin. AIF-1 is useful for diagnosing and treating allograft rejection
 CC and other conditions associated with vascular inflammation, especially
 CC atherosclerosis. The present sequence represents a PCR primer which is
 CC used in an example from the present invention
 XX CC
 XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGCTGGC 14
 Db 9 TCGCTGGC 2
 RESULT 152
 AAH63243
 ID AAH63243 standard; cDNA; 10 BP.
 XX AC
 XX AAH63243;
 XX DT
 XX 20-SEP-2001 (first entry)
 XX DE
 XX Human colon epithelium specific transcriptome sequence SEQ ID NO: 83.
 XX KW
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX OS
 XX Homo sapiens.
 XX PN
 XX WO200138577-A2.
 XX PD
 XX 31-MAY-2001.
 XX PF
 XX 21-NOV-2000; 2000MO-US031922.
 XX PR
 XX 24-NOV-1999; 99US-00448480.
 XX PA
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX PI
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 XX DR
 XX WPI; 2001-367706/38.
 XX PT
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX OS
 XX Claim 11; Page 40; 94pp; English.
 XX PS
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention

XX
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
| | | | |
Db 3 ATGGACTC 10

RESULT 153
AAF33482/c
ID AAF33482 standard; DNA; 10 BP.
XX
AC AAF33482;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:221.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 26; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate phases which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
| | | | |
Db 10 GCACGCAC 3

RESULT 154
AAF38218/c
ID AAF38218 standard; DNA; 10 BP.
XX
AC AAF38218;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4957.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 177; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate phases which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 5 ACTCGCTG 12
 |||||
 Db 10 ACTCGCTG 3

RESULT 155
 AAF40202
 ID AAF40202 standard; DNA; 10 BP.

XX AAF40202;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 247; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 ATGGAATC 8
 |||||
 Db 1 ATGGAATC 8

RESULT 156

AAF37632

ID AAF37632 standard; DNA; 10 BP.

XX AAF37632;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4371.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 156; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GACTCGCT 11
 |||||
 Db 1 GACTCGCT 8

RESULT 157
 AAF37418/c
 ID AAF37418 standard; DNA; 10 BP.

AC AAF37418;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4157.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

PS Example; Page 148; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 GCACGCAC 20
 |||||
 Db 10 GCACGCAC 3

RESULT 158
 AAF40866/c
 ID AAF40866 standard; DNA; 10 BP.

XX AAF40866;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7605.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

PS Example; Page 271; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast

cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTCGCTGG 13
DB 8 CTCGCTGG 1

RESULT 159
AAH77187/C
ID AAH77187 standard; DNA; 10 BP.

XX AC AAH77187;
XX DT 24-JAN-2002 (first entry)
XX DE Rat arbitrary PCR primer AP-1.

XX KW Rat; oestrogen agonist-inducible; hUO-44; cytostatic; ovary;
XX KW uterine cancer; ovarian cancer; uterine growth; uterine; development;
XX KW ovarian growth; ovarian development; oestrogenic activity; PCR primer;
XX KW AP-1; ss.

XX OS Rattus norvegicus.

XX PN WO200175099-A1.

XX PD 11-OCT-2001.

XX PF 04-APR-2001; 2001WO-AU000379.

XX PR 04-APR-2000; 2000US-0194566P.

XX PR 15-AUG-2000; 2000AU-00009471.

XX PA (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.

XX PA (HUGH/) HUGHES E U L.

XX PI Huynh TH;

XX DR WPI; 2002-010789/01.

XX PT Novel isolated UO-44 nucleic acid molecule useful for treating or

XX PT diagnosing uterine and/or ovarian cancers, comprises sequence

XX PT corresponding to uterine estrogen agonist-inducible genetic sequence in

XX PT mammal.

XX PS Example 2; Page 37; 82pp; English.

XX PS The sequence represents the rat arbitrary PCR primer AP-1, used in the
XX CC invention to amplify cDNA from rat ovary tissue. The invention relates to
XX CC a novel isolated UO-44 nucleic acid molecule comprising a sequence of

CC nucleotides corresponding to a uterine oestrogen agonist-inducible
CC genetic sequence in a mammal. The UO-44 sequences of the invention have
CC cytostatic activity. The UO-44 polynucleotide is useful in the
CC manufacture of a medicament for the treatment of a condition in a mammal,
CC for treating, diagnosing, detecting or monitoring uterine cancers and/or
CC ovarian cancers, and for producing the polypeptide. The polynucleotide or
CC polypeptide is useful for monitoring uterine and ovarian growth and
CC development and the level of oestrogenic activity in tissue including
CC cancer tissue. They are also useful for the generation of a range of
CC therapeutic molecules capable of modulating oestrogen agonist-mediated
CC cell growth and proliferation in the uterus including ovaries. The UO-44
CC polypeptide is useful to screen for naturally occurring antibodies to
CC itself

SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TCGCTGGC 14
DB 9 TCGCTGGC 2

RESULT 160

AAAD26026/C

ID AAD26026 standard; DNA; 10 BP.

XX AC AAD26026;

XX DT 26-MAR-2002 (first entry)

XX DE Primer #28 to detect human PI4 gene polymorphisms.

XX KW Human; protease inhibitor; PI4; kallistatin; therapy; polymorphic site;
XX KW PS; haplotyping; genotyping; acute pancreatitis; drug screening;
XX KW antiinflammatory; chromosome 14q31-q32.1; primer; ss.

XX OS Homo sapiens.

XX FN WO200179227-A2.

XX XX 25-OCT-2001.

XX PF 13-APR-2001; 2001WO-US012255.

XX PR 13-APR-2000; 2000US-0196990P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX XX Choi JY, Koshy B, Sanchis A;

XX DR WPI; 2002-075060/10.

XX PT Genotyping protease inhibitor 4 gene of individual for determining
XX PT haplotype of individual, involves determining identity of nucleotide pair
XX PT at specific polymorphic sites for two copies of gene.

XX PS Claim 18; Page 14; 79pp; English.

XX CC The present invention relates to genotyping protease inhibitor (PI) 4
XX CC (kallistatin) gene of an individual, involves determining for the two
XX CC copies of the PI4 gene present in the individual, the identity of the
XX CC nucleotide pair at one or more polymorphic sites. PI4 gene is located on
XX CC chromosome 14q31-q32.1. Genotyping is useful for determining if an
XX CC individual has a haplotype or haplotype pairs defined in the
XX CC specification. Haplotyping is useful for improving the efficacy and
XX CC reliability of several steps in the discovery and development of drugs
XX CC for treating diseases associated with PI4 activity, e.g. acute
XX CC pancreatitis, to validate PI4 as a candidate agent for treating a
XX CC specific condition or disease predicted to be associated with PI4
XX CC activity, and in the design of clinical trials of candidate drugs for

CC treating a specific condition or disease predicted to be associated with
CC P14 activity. The P14 gene is useful in studying the expression and
CC function of P14, and in expressing P14 protein for use in screening for
CC candidate drugs to treat diseases related to P14 activity. The present
CC sequence is a primer to detect human P14 gene polymorphisms
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCAC 16
Db 10 GCTGGCAC 3

RESULT 161
AAL42350/C
ID AAL42350 standard; DNA; 10 BP.
XX AC AAL42350;
XX DT 28-JUN-2002 (first entry)
XX DE Novel sand pear microsatellite DNA PCR primer 14.
XX KW Sand pear; ss; PCR; primer; novel microsatellite DNA sequence;
XX PYrus plant discrimination.
XX OS Pyrus pyrifolia.
XX JN JP2002034597-A.
XX PD 05-FEB-2002.
XX PF 21-JUL-2000; 2000JP-00220339.
XX PR 21-JUL-2000; 2000JP-00220339.
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX DR WPI; 2002-298819/34.
XX PT A new microsatellite DNA derived from a Pyrus plant and discrimination of
XX Pyrus plants by using it.
XX PS Example 1; Page 5; 22pp; Japanese.
XX CC The invention comprises a novel microsatellite DNA sequence derived from
XX Pyrus plants. The invention also comprises a method for discriminating
XX Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel
XX microsatellite DNA sequence can be used in discriminating Pyrus plants.
XX CC The present DNA sequence represents a PCR primer specific for a novel
XX Pyrus pyrifolia (sand pear) microsatellite DNA sequence
XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCCTGGC 14
Db 9 TCCTGGC 2

RESULT 162
ABK68734
ID ABK68734 standard; DNA; 10 BP.
XX AC ABK68734;
XX DE

CC treating a specific condition or disease predicted to be associated with
CC P14 activity. The P14 gene is useful in studying the expression and
CC function of P14, and in expressing P14 protein for use in screening for
CC candidate drugs to treat diseases related to P14 activity. The present
CC sequence is a primer to detect human P14 gene polymorphisms
XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTCGCT 11
Db 1 GACTCGCT 8

RESULT 163
ACF12803/C
ID ACF12803 standard; DNA; 10 BP.
XX AC ACF12803;
XX DT 09-SEP-2003 (first entry)
XX DE Primer used during DDPCR analysis #20.

CC The present invention relates to a new polynucleotide with a sequence
CC comprising an olfactory receptor, family 11, subfamily A, member 1
CC (OR11A1) isogene selected from 9 isogenes, with regions of a fully
CC defined 8980 base pair sequence given in the specification. The
CC polynucleotide is also defined by a corresponding set of polymorphisms
CC whose locations are given in the specification. The invention is useful
CC for haplotyping and genotyping the OR11A1 gene in an individual. Other
CC uses include predicting a haplotype pair for OR11A1 gene of an
CC individual, and for identifying an association between a trait and at
CC least one haplotype pairs or haplotypes of OR11A1 gene. The polypeptide
CC is also useful in studying the expression and function of OR11A1, and in
CC expressing OR11A1 protein for use in screening for candidate drugs to
CC treat diseases related to OR11A1 activity and in studying the effect of
CC the variation on the biological activity of OR11A1 as well as on the
CC binding affinity of candidate drugs targeting OR11A1 for the treatment of
CC olfactory disorders. Without requiring any prior knowledge of the
CC phenotypic effect of any particular OR11A1 haplotype pair of haplotypes,
CC the method of the invention provides the scientist with a tool to
CC identify lead compounds that are more likely to show efficacy in clinical
CC trials. The present nucleic acid sequence represents one of a collection
CC of oligonucleotide primers (ABK68729- ABK68744) that were used in the
CC invention to detect polymorphisms in the human OR11A1 gene
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTCGCT 11
Db 1 GACTCGCT 8

RESULT 163
ACF12803/C
ID ACF12803 standard; DNA; 10 BP.
XX AC ACF12803;
XX DT 09-SEP-2003 (first entry)
XX DE Primer used during DDPCR analysis #20.

XX Endometrium; placenta; serine protease; gynecological; cytostatic;
 KW cardiant; PRSP; infertility; endometriosis; cancer; pregnancy; primer;
 KW PCR; ss.
 XX Synthetic.
 XX WO2003011905-A1.
 PN 13-FEB-2003.
 XX 30-JUL-2003; 2002WO-AU001010.
 PF 30-JUL-2001; 2001AU-00006707.
 PR (PRIN-) PRINCE HENRY'S INST MEDICAL RES.
 XX
 PI Nie G, Salamonsen LA, Li Y, Hampton AL, Findlay JK;
 XX WPI; 2003-268108/26.
 DR
 XX New nucleic acid encoding a protein having serine protease activity and
 PT an insulin-like growth factor-binding motif, useful for preparing a
 PF composition for treating a pregnancy-related serum protease-related
 XX condition e.g., infertility.
 PT
 XX Example 1; Page 55; 156pp; English.
 PS
 XX The present sequence relates to a new isolated nucleic acid molecule,
 CC which is expressed in endometrium and placenta and is upregulated in
 CC pregnant uterus and is highly expressed during placental development,
 CC encodes a protein having serine protease activity and has an insulin-like
 CC growth factor (IGF)-binding motif. The compound is considered
 CC gynecological, cytostatic and cardiant. The enzyme is specifically
 CC expressed in association with embryo implantation and placenta in a
 CC pregnant uterus. The nucleic acid is useful for preparing a composition
 CC for treating PRSP-related condition e.g., infertility, endometriosis,
 CC cancer or a disease of the heart, testis or ovaries. Further, it is
 CC useful for detecting, diagnosing or monitoring a condition involving a
 CC change in PRSP expression. The sequence is present in the exemplification
 CC of the specification
 XX
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TCGCTGGC 14
 Db 9 TCGCTGGC 2
 XX
 RESULT 164
 ACA94640
 ID ACA94640 standard; DNA; 10 BP.
 XX
 AC ACA94640;
 XX
 XX 18-JUL-2003 (first entry)
 XX
 XX DNA tag from human transcript repressed in adenomas/cancers #173.
 XX
 XX Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 XX WO2003022863-A1.
 PN 20-MAR-2003.
 PD
 XX

PF 09-SEP-2002; 2002WO-US028518.
 XX
 XX 07-SEP-2001; 2001US-0317494P.
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Buckhaults P, Kinzler KW, Vogelstein B;
 PI WPI; 2003-313220/30.
 XX
 DR
 XX Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 XX Disclosure; Page 31; 59pp; English.
 PS
 XX The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces, by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCTGGCAC 16
 Db 1 GCTGGCAC 8
 XX
 RESULT 165
 AAX05787
 ID AAX05787 standard; DNA; 11 BP.
 XX
 AC AAX05787;
 XX
 XX 29-APR-1999 (first entry)
 XX
 XX Incorrectly called sequence by intensity ratio method.
 XX

KW Computer system; nucleic acid analysis; fluorescence intensity;
 KW hybridized; nucleic acid probe; mutation identification; mutant;
 KW intensity ratio; ss.

OS Unidentified.

XX EP171113-A2.

PD 19-JUN-1996.

XX 20-OCT-1995; 95EP-00307476.

XX 21-OCT-1994; 94US-00327525.

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

PI Chee MS, Wang C, Jevons LC, Bernhart DH, Lipshutz RJ;

XX WPI; 1996-279562/29.

PT Identification of unknown base in nucleic acid sequence - using computer
 PT system to compare sequences by fluorescent intensities.

PS Disclosure; Page 45; 78pp; English.

XX The invention relates to a computer system for analysing nucleic acid
 CC sequences. The computer system is used to perform multiple methods for
 CC determining unknown bases by analysing the fluorescence intensities of
 CC hybridized nucleic acid probes. The results of individual experiments may
 CC be improved by processing nucleic acid sequences together. Comparative
 CC analysis of multiple experiments is also provided by displaying reference
 CC sequences in one area and sample sequences in another area on a display
 CC device. The computer system is also used to identify mutations in a
 CC sample nucleic acid. Sequences AAX05784-787 represent sequences with
 CC mutant bases that were incorrectly called by the intensity ratio method

SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGGCAGC 17

Db 1 CTGGCAGC 8

RESULT 166

AAZ19002/c
 ID AAZ19002 standard; DNA; 11 BP.

AC AAZ19002;

XX 22-OCT-1999 (first entry)

DE Murine MRL SAGE tag 3008230.

XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.

OS Mus sp.

XX WO9941364-A2.

PD 19-AUG-1999.

XX 12-FEB-1999; 99WO-US002962.

PR 13-FEB-1998; 98US-0074737P.

PR 26-AUG-1998; 98US-0087937P.

PR 28-SEP-1998; 98US-0102051P.

XX

PA (WIST-) WISTAR INST.

XX Heber-Katz E;

XX WPI; 1999-494533/41.

XX New mammalian model for enhanced wound healing - useful for identifying
 PT enhanced wound healing genes.

XX Claim 13; Page 74; 136pp; English.

XX This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention

SQ Sequence 11 BP; 0 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCA 19

Db 11 GGCACGCA 4

RESULT 167

AAZ23069
 ID AAZ23069 standard; DNA; 11 BP.

XX AAZ23069;

XX 17-JAN-2000 (first entry)

XX Seq ID No: 39 of US974164.

XX Mutation; fluorescent intensity; probe intensity; hybridization;
 KW cystic fibrosis; P53 gene; cancer; HIV; genetic characteristic; ss.

XX Synthetic.

XX US5974164-A.

XX 26-OCT-1999.

XX 16-OCT-1995; 95US-00531137.

XX 21-OCT-1994; 94US-00327525.

XX (AFFY-) AFFYMETRIX INC.

XX Chee MS;

XX WPI; 1999-610467/52.

XX Identification of mutation in nucleic acid sample using a computer aided
 PT system.

XX

PS Disclosure; Fig 20; 59pp; English.

XX The invention provides a method of identifying mutations in sample

CC nucleic acid, by analyzing fluorescent intensities of hybridized nucleic

CC acid probes using a computer system. The method comprises: (a) inputting

CC a first set of probe intensities, each of the probe intensities is

CC associated with a nucleic acid probe, indicating hybridization affinity

CC between the associated nucleic acid probe and a reference nucleic acid

CC sequence; (b) inputting a second set of probe intensities, each of the

CC probe intensities is associated with a nucleic acid probe and indicating

CC hybridization affinity between the associated nucleic acid probe and the

CC sample sequences; (c) the computer system comparing probe intensities in

CC the first set and probe intensities in the second set to select

CC hybridization regions where the probe intensities in the first set and

CC the probe intensities in the second set differ, with each region

CC including multiple base positions; and (d) identifying mutations in the

CC sample sequence according to characteristics of the selected regions.

CC Based upon the image file and identities of the probes at specific

CC locations, it becomes possible to extract information such as the monomer

CC sequence of DNA, or RNA. Such systems can be used to form e.g. arrays of

CC DNA that may be used to study and detect mutations relevant to cystic

CC fibrosis, the P53 gene (relevant to certain cancers), HIV, and other

CC genetic characteristics. This computer-aided system allows researchers to

CC analyze, evaluate, and process the vast amounts of information now used

CC and made available by pioneering technologies

XX

SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CTGGCAGC 17

Db 1 CTGGCAGC 8

RESULT 168

AAF90178

ID AAF90178 standard; DNA; 11 BP.

XX

AC AAF90178;

XX

DT 06-AUG-2001 (first entry)

XX

DE DNA sequence used in a computer implemented method.

XX

KW Mutation; cystic fibrosis; P53 gene; cancer; HIV; protease gene;

KW human immunodeficiency virus; ss.

XX

OS Synthetic.

XX

PN US6242180-B1.

XX

PD 05-JUN-2001.

XX

PF 23-SEP-1998; 98US-00158765.

XX

PR 21-OCT-1994; 94US-00327525.

PR 16-OCT-1995; 95US-00531137.

XX

PA (AFFY-) AFFYMETRIX INC.

XX

PI Chee MS;

XX

PI WPI; 2001-373810/39.

XX

PT Computer implementation for calling unknown bases in a sample nucleic

PT acid sequence involves calling bases according to probe intensities,

PT identifying mutant base call, and analyzing probe intensities near

PT suspected mutation.

XX

PS Disclosure; Col 49; 59pp; English.

XX The specification describes a computer implemented method of calling

CC unknown bases in a sample nucleic acid sequence. The method comprises

CC calling bases of the sample nucleic acid sequence according to inputted

CC probe intensities, identifying a mutant base call, analysing probe

CC intensities of positions near the suspected mutation, and changing the

CC mutant base call to nonmutant base call if probe intensities are

CC inconsistent of a mutation. The method is used to study and detect

CC mutations relevant to cystic fibrosis, the P53 gene (relevant to certain

CC cancers), human immunodeficiency virus, and other genetic

CC characteristics. The present sequence is used in the course of the

CC invention

XX

SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CTGGCAGC 17

Db 1 CTGGCAGC 8

RESULT 169

ABQ87673/C

ID ABQ87673 standard; cDNA; 11 BP.

XX

AC ABQ87673;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human skin stress/ageing related EST SEQ ID NO 1428.

XX

KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN WO200253773-A2.

XX

PD 11-JUL-2002.

XX

PF 20-DEC-2001; 2001WO-EP015178.

XX

PR 03-JAN-2001; 2001DE-01000121.

XX

PA (HENK) HENKEL KGAA.

XX

PI Petersohn D, Conradt M, Hofmann K;

XX

PI WPI; 2002-528865/56.

XX

PT Identifying genes involved in skin stress and aging, useful e.g. in

PT screening for cosmetic or therapeutic agents, based on differential gene

PT expression.

XX

PS Claim 8; Page 98; 325pp; German.

XX

CC The invention relates to identifying (M1) genes in vitro that, in humans

CC or animals, are important for skin ageing and/or skin stress by serial

CC analysis of gene expression between mixtures of transcribed and

CC optionally translated, genetically encoded factors (A) obtained from

CC young and aged skin, to identify that genes that show strong differential

CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is

CC useful for: identifying markers of skin ageing and/or stress; determining

CC skin ageing and/or stress; and identifying or determining the effects of

CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed

CC sequence tags (ABQ86246-ABQ87680) of the invention

XX

SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
 Db 11 ATGGACTC 4

RESULT 170
 ABQ86610/c
 ID ABQ86610 standard; cDNA; 11 BP.
 XX
 AC ABQ86610;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 365.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 screening for cosmetic or therapeutic agents, based on differential gene
 expression.
 XX
 PS Claim 8; Page 51; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 or animals, are important for skin ageing and/or skin stress by serial
 analysis of gene expression between mixtures of transcribed and
 optionally translated, genetically encoded factors (A) obtained from
 young and aged skin, to identify that genes that show strong differential
 expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 useful for: identifying markers of skin ageing and/or stress; determining
 skin ageing and/or stress; and identifying or determining the effects of
 pharmaceutical or cosmetic agents for control of skin ageing. The present
 sequence is one of a group of human skin ageing/stress related expressed
 sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8
 Db 10 ATGGACTC 3

RESULT 171
 ABQ87096/c
 ID ABQ87096 standard; cDNA; 11 BP.
 XX
 AC ABQ87096;
 XX
 DT 10-SEP-2002 (first entry)
 XX

DE Human skin stress/ageing related EST SEQ ID NO 851.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 screening for cosmetic or therapeutic agents, based on differential gene
 expression.
 XX
 PS Claim 8; Page 72; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 or animals, are important for skin ageing and/or skin stress by serial
 analysis of gene expression between mixtures of transcribed and
 optionally translated, genetically encoded factors (A) obtained from
 young and aged skin, to identify that genes that show strong differential
 expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 useful for: identifying markers of skin ageing and/or stress; determining
 skin ageing and/or stress; and identifying or determining the effects of
 pharmaceutical or cosmetic agents for control of skin ageing. The present
 sequence is one of a group of human skin ageing/stress related expressed
 sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCGCTGG 13
 Db 11 CTCGCTGG 4

RESULT 172
 ABQ87629/c
 ID ABQ87629 standard; cDNA; 11 BP.
 XX
 AC ABQ87629;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 1384.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX

PI Petersohn D, Conradt M, Hofmann K;
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX
 PS Claim 8; Page 96; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 Db |||||
 11 GCACGCAC 4
 RESULT 173
 ABV68894/C
 ID ABV68894 standard; cDNA; 11 BP.
 XX
 AC ABV68894;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 6680.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 PS WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 211; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC

CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGACTC 8
 Db |||||
 10 ATGGACTC 3
 RESULT 174
 ABV64169
 ID ABV64169 standard; cDNA; 11 BP.
 XX
 AC ABV64169;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1955.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 PS WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 79; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGCG 18
 | | | | | | | |
 Db 1 TGGCAGCG 8

RESULT 175
 ABV67742/c
 ID ABV67742 standard; cDNA; 11 BP.
 XX
 AC ABV67742;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 5528.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 DT 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 177; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCGCTGG 13
 | | | | | | | |
 Db 11 CTCGCTGG 4

RESULT 176
 ABV62329
 ID ABV62329 standard; cDNA; 11 BP.
 XX
 AC ABV62329;
 XX

DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 115.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 DT 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 29; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGCG 18
 | | | | | | | |
 Db 2 TGGCAGCG 9

RESULT 177
 ABV71734/c
 ID ABV71734 standard; cDNA; 11 BP.
 XX
 AC ABV71734;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 9520.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 DT 11-JUL-2002.

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 |||||
 Db 11 GCACGCAC 4
 RESULT 180
 ABV72049/c
 ID ABV72049 standard; cDNA; 11 BP.
 XX AC ABV72049;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 9835.
 XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX KW WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX KW In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Claim 24; Page 319; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGACTC 8
 |||||
 Db 11 ATGGACTC 4

RESULT 181
 ABV68016/c
 ID ABV68016 standard; cDNA; 11 BP.
 XX AC ABV68016;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 5802.
 XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX KW In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 185; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GGCACGCA 19
 |||||
 Db 11 GGCACGCA 4
 RESULT 182
 ABV69750
 ID ABV69750 standard; cDNA; 11 BP.
 XX AC ABV69750;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 7536.
 XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;

KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 OS Homo sapiens.
 PN WO200253774-A2.
 XX 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 DR homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 PS Claim 24; Page 238; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGCGACGC 18
 Db 2 TGCGACGC 9
 RESULT 183
 ABV63949/C
 ID ABV63949 standard; cDNA; 11 BP.
 AC ABV63949;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 1735.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antisborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX The invention relates to in vitro identification (M1) of genes expressed

PA (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 DR homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 PS Disclosure; Page 72; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 Db 11 GCACGCAC 4
 RESULT 184
 ABV65067
 ID ABV65067 standard; cDNA; 11 BP.
 AC ABV65067;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 2853.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antisborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 DR homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 PS Disclosure; Page 104; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 CC
 SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCAC 16
 Db 3 GCTGGCAC 10
 |||||

RESULT 185

ABV71370/c
 ID ABV71370 standard; cDNA; 11 BP.

XX AC ABV71370;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 9156.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Claim 24; Page 294; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 CC

SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
 Db 11 GCACGCAC 4
 |||||

RESULT 186

ABV64955/c
 ID ABV64955 standard; cDNA; 11 BP.

XX AC ABV64955;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 2741.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 101; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 CC

SQ Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
 Db 8 ATGGACTC 1
 |||||

RESULT 187

ABV68998
 ID ABV68998 standard; cDNA; 11 BP.

XX AC ABV68998;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 6784.
 XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
 XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX PS Disclosure; Page 213; 1345pp; German.
 XX SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 CC Query Match 40.0%; Score 8; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGGACTCG 9
 DB 3 TGGACTCG 10
 RESULT 188
 ABV71590
 ID ABV71590 standard; cDNA; 11 BP.
 XX AC ABV71590;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 9376.
 XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
 XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.

PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX PS Claim 24; Page 302; 1345pp; German.
 XX SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 CC Query Match 40.0%; Score 8; DB 1; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TGGCAGCC 18
 DB 1 TGGCAGCC 8
 RESULT 189
 ABK47234
 ID ABK47234 standard; DNA; 11 BP.
 XX AC ABK47234;
 XX DT 05-JUN-2002 (first entry)
 XX DE Nucleic acid analysis computer system, oligonucleotide #39.
 XX KW Nucleic acid analysis; computer analysis; ss.
 XX OS Synthetic.
 XX PN US2002012925-A1.
 XX PD 31-JAN-2002.
 XX PF 27-FEB-2001; 2001US-00796071.
 XX PR 21-OCT-1994; 94US-00327525.
 XX PR 16-OCT-1995; 95US-00531137.
 XX PR 23-SEP-1998; 98US-00158765.
 XX PA (CHEE/) CHEE M S.
 XX PI Chee MS;
 XX DR WPI; 2002-205097/26.

XX Computer aided method of identifying unknown base in sample nucleic acid
PT sequence, comprises analyzing the fluorescence intensities of nucleic
PT acid probes hybridized with at least one sample nucleic acid sequence.
XX
XX Disclosure; Fig 20; 53pp; English.
XX
XX The invention described a computer system for identifying an unknown base
in a sample nucleic acid sequence. The method comprises analyzing the
XX fluorescence intensities of nucleic acid probes hybridized with at least
XX one sample nucleic acid sequence. The computer system is useful for
XX visualizing, evaluating, and comparing biological sequences, for
XX analysing fluorescent image files of a chip containing hybridised nucleic
XX acid probes to call bases in a sample of nucleic acid sequences, and for
XX identifying an unknown base in a sample nucleic acid sequence. This
XX sequence represents an oligonucleotide used to demonstrate the nucleic
XX acid analysis system described in the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 190
AA54872
ID AAX54872 standard; DNA; 12 BP.
XX
AC AAX54872;
XX
DT 05-JUL-1999 (first entry)
XX
DE C/EBP-beta antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
OS Synthetic.
XX
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX
XX 03-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
XX Disclosure; Page 67; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAX52869-X55271)

CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
SQ Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CTGCTGG 13
Db 1 CTGCTGG 8

RESULT 191
AAX34405
ID AAX34405 standard; DNA; 12 BP.
XX
AC AAX34405;
XX
DT 25-JUN-1999 (first entry)
XX
DE Template sequence Seq ID No: 5.
XX
XX Rolling template; nucleic acid synthesis; polynucleotide polymerase;
XX gene production; primer; ss.
XX
OS Synthetic.
XX
XX WO9914370-A1.
XX
XX 25-MAR-1999.
XX
XX 15-SEP-1998; 98WO-US019157.
XX
XX 15-SEP-1997; 97US-00929856.
XX
XX (HIAT/) HIATT A C.
XX (ROSE/) ROSE F D.
XX
XX Hiatt AC, Rose FD;
XX
XX WPI; 1999-244045/20.
XX
XX Producing specific polynucleotides using rolling templates.
XX
XX Disclosure; Page 25; 109pp; English.
XX
XX The invention relates to a method for producing polynucleotides having a
XX defined sequence using rolling templates that successively add
XX nucleotides (nts) to a longer primer strand. The method comprises: (i)
XX incubating, under annealing conditions, a primer and a template that has
XX a 5'-region not complementary to the primer, a 3'-region complementary to
XX the 3'-end of primer and a non-reactive 3'-terminus, with the template
XX being shorter than the primer; (ii) reacting the primer with at least one
XX nt in presence of a template-dependent polynucleotide polymerase to

CC extend it by at least one nt (complementary to the 5'-region of template)
 CC at its 3'-end; (iii) separating the template and the extended primer; and
 CC (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize
 CC the desired polynucleotide. The method is especially used to produce
 CC genes or their segments. The method provides fast, accurate, inexpensive
 CC syntheses of RNA or DNA and is more efficient than chemical coupling
 CC processes. It has higher specificity and eliminates the need for
 CC deprotection. The products can be cloned directly. The method avoids
 CC problems of waste disposal and includes an inherent editing effect
 CC (failure sequences will not be extended further in subsequent rounds) so
 CC that purification of the end product is facilitated. Synthesis may take
 CC place on a vector, simplifying cloning and sequences with codon usage
 CC optimized for a particular host can be prepared

XX
 SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGACTC 8

Db 5 ATGGACTC 12
 |||||

RESULT 192

AAA34319
 ID AAA34319 standard; DNA; 12 BP.

XX
 AC AAA34319;

XX
 DT 28-JUL-2000 (first entry)

XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2008.

XX
 KW Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX
 OS Homo sapiens.

XX
 PN WO200009525-A2.

XX
 PD 24-FEB-2000.

XX
 PF 03-AUG-1999; 99WO-US017712.

XX
 PR 03-AUG-1998; 98US-0095212P.

XX
 PA (UYEC-) UNIV EAST CAROLINA.

XX
 PI Nyce JW;

XX
 DR WPI; 2000-205971/18.

XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

XX
 PS Disclosure; Page 517; 1343pp; English.

XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1880 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTGCTGG 13

Db 1 CTGCTGG 8
 |||||

RESULT 193

AAF20441

ID AAF20441 standard; DNA; 12 BP.

XX
 AC AAF20441;

XX
 DT 14-MAR-2001 (first entry)

XX
 DE Human C/EBP polynucleotide fragment #2008.

XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX
 OS Homo sapiens.

XX
 PN WO200062736-A2.

XX
 PD 26-OCT-2000.

XX
 PF 24-MAR-2000; 2000WO-US008020.

XX
 PR 06-APR-1999; 99US-0127958P.

XX
 PA (UYEC-) UNIV EAST CAROLINA.

XX
 PI (NYCE/) NYCE J W.

XX
 DR WPI; 2000-679539/66.

XX
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

PS Claim 14; Page 261; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with the
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCGCTGG 13
 Db 1 CTCGCTGG 8
 |||||

RESULT 194
 ABH86538
 ID ABH86538 standard; DNA; 12 BP.
 AC ABH86538;
 XX
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 286531 for detecting SNP TSC0012735.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 FN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 286531; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABP0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCACGCAC 20
 Db 4 GCACGCAC 11
 |||||

RESULT 195
 ABI10644/C
 ID ABI10644 standard; DNA; 12 BP.
 AC ABI10644;
 XX
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 310617 for detecting SNP TSC0024025.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 FN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 310617; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 DB 10 GCACGCAC 3
 RESULT 196
 ABH86548
 ID ABH86548 standard; DNA; 12 BP.
 XX
 AC ABH86548;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 286541 for detecting SNP TSC0012735.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 286541; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20

DB 4 GCACGCAC 11
 RESULT 197
 ABI10603/C
 ID ABI10603 standard; DNA; 12 BP.
 XX
 AC ABI10603;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 310576 for detecting SNP TSC0024024.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 310576; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 DB 10 GCACGCAC 3
 RESULT 198
 ABI23926
 ID ABI23926 standard; DNA; 12 BP.
 XX
 AC ABI23926;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 323899 for detecting SNP TSC0031670.

XX	XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS	OS	Homo sapiens.
XX	XX	
PN	PN	WO200177384-A2.
PD	PD	18-OCT-2001.
XX	XX	
PF	PF	06-APR-2001; 2001WO-IB000713.
XX	XX	
PR	PR	07-APR-2000; 2000DE-01019173.
XX	XX	(EPiG-) EPIGENOMICS AG.
XX	XX	Olek A, Piepenbrock C, Berlin K;
PI	PI	WPI; 2001-657177/75.
XX	XX	
DR	DR	Set of oligonucleotides, useful for diagnosis and cell typing, is
XX	XX	designed to detect single-nucleotide polymorphisms and cytosine
PT	PT	methylation status.
XX	XX	
PS	PS	Claim 1; SEQ ID NO 323899; 29bp + Sequence Listing; German.
XX	XX	
CC	CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	CC	central nervous system, cardiovascular and metabolic disorders. The
CC	CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073
CC	CC	represent the oligomers described in the invention. NOTE: the sequence
CC	CC	data for this patent did not form part of the printed specification, but
CC	CC	was obtained in electronic format from WIPO at
XX	XX	ftp.wipo.int/pub/published_pct_sequences
XX	XX	
SQ	SQ	Sequence 12 BP; 3 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
		Query Match 40.0%; Score 8; DB 1; Length 12;
		Best Local Similarity 100.0%; Pred.No. 1.3e+02;
		Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	QY	13 GCACGCAC 20
Db	Db	2 GCACGCAC 9
RESULT 199		
ABH86551	ID	ABH86551 standard; DNA; 12 BP.
XX	XX	ABH86551;
AC	AC	
XX	XX	
DT	DT	22-FEB-2002 (first entry)
XX	XX	
DE	DE	Oligonucleotide primer SEQ ID NO 286544 for detecting SNP TSC0012735.
XX	XX	
KW	KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	
PN	PN	WO200177384-A2.
XX	XX	
PD	PD	18-OCT-2001.
XX	XX	
PF	PF	06-APR-2001; 2001WO-IB000713.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db |||||

RESULT 201
ABI10579
ID ABI10579 standard; DNA; 12 BP.
XX AC ABI10579;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 310552 for detecting SNP TSC0024024.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 310552; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db 3 GCACGCAC 10
|||

RESULT 202
ABI10573
ID ABI10573 standard; DNA; 12 BP.
XX AC ABI10573;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 310546 for detecting SNP TSC0024024.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 310546; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db 3 GCACGCAC 10
|||

RESULT 203

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ABH86561
ID ABH86561 standard; DNA; 12 BP.
AC ABH86561;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 286554 for detecting SNP TSC0012735.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286554; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Claim 1; SEQ ID NO 286554; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db |||||
4 GCACGCAC 11
RESULT 204
ABH86571
ID ABH86571 standard; DNA; 12 BP.
XX
XX ABH86571;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 286564 for detecting SNP TSC0012735.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286554; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db |||||
4 GCACGCAC 11
RESULT 204
ABH86571
ID ABH86571 standard; DNA; 12 BP.
XX
XX ABH86571;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 286564 for detecting SNP TSC0012735.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286554; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db |||||
4 GCACGCAC 11
RESULT 205
ABH10639/c
ID ABH10639 standard; DNA; 12 BP.
XX
XX ABH10639;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 310612 for detecting SNP TSC0024025.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;

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OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286564; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db |||||
4 GCACGCAC 11
RESULT 205
ABH10639/c
ID ABH10639 standard; DNA; 12 BP.
XX
XX ABH10639;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 310612 for detecting SNP TSC0024025.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;

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XX 06-APR-2001; 2001WO-IB000713.
PF 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 286498; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
DB 11 GCACGCAC 4
RESULT 211
ABH86541
ID ABH86541 standard; DNA; 12 BP.
XX AC ABH86541;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 286534 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 286498; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
DB 11 GCACGCAC 4
RESULT 211
ABH86541
ID ABH86541 standard; DNA; 12 BP.
XX AC ABH86541;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 286534 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
XX Claim 1; SEQ ID NO 286534; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
DB 2 GCACGCAC 9
RESULT 212
ABH86479/C
ID ABH86479 standard; DNA; 12 BP.
XX AC ABH86479;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 286472 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 286472; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db 11 GCACGCAC 4

RESULT 213
ABH86489/c
ID ABH86489 standard; DNA; 12 BP.
XX AC ABH86489;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286482 for detecting SNP TSC0012735.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 286482; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db 11 GCACGCAC 4

RESULT 214
ABH86567
ID ABH86567 standard; DNA; 12 BP.
XX AC ABH86567;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286560 for detecting SNP TSC0012735.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 286560; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 2 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
Db 2 GCACGCAC 9

RESULT 215
AB144927/c
ID AB144927 standard; DNA; 12 BP.
XX AC AB144927;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 344900 for detecting SNP TSC0043755.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 344900; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 DB 10 GCACGCAC 3
 RESULT 216
 ABI10609/c
 ID ABI10609 standard; DNA; 12 BP.
 XX
 AC ABI10609;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 310582 for detecting SNP TSC0024024.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 286479; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic

(EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 310582; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 DB 10 GCACGCAC 3
 RESULT 217
 ABH86486/c
 ID ABH86486 standard; DNA; 12 BP.
 XX
 AC ABH86486;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 286479 for detecting SNP TSC0012735.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 286479; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
 Db 9 GCACGCAC 2

RESULT 218
 ABH10600/C
 ID ABH10600 standard; DNA; 12 BP.

XX AC ABH10600;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 310573 for detecting SNP TSC0024024.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB0000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 310573; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

XX SQ Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
 Db 8 GCACGCAC 1

RESULT 219
 ABH86476/C
 ID ABH86476 standard; DNA; 12 BP.

XX AC ABH86476;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 286469 for detecting SNP TSC0012735.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB0000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 286469; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

XX SQ Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20
 Db 9 GCACGCAC 2

RESULT 220
 ABH10630
 ID ABH10630 standard; DNA; 12 BP.

XX AC ABI10630;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 310603 for detecting SNP TSC0024025.
 XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX DT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX CS Claim 1; SEQ ID NO 310603; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -AB00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 GCACGCAC 20
 Db 5 GCACGCAC 12
 RESULT 221
 ABZ96135
 ID ABZ96135 standard; DNA; 12 BP.
 XX AC ABZ96135;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human C/EBP antisense fragment no.1995.
 XX DE Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytosine; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX DR WPI; 2003-229219/22.
 XX CC Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Disclosure; SEQ ID NO 11377; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
 CC receptor producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CTCGCTGG 13
 Db 1 CTCGCTGG 8
 RESULT 222
 AAQ53920/c
 ID AAQ53920 standard; DNA; 11 BP.
 XX AC AAQ53920;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-JUN-1994 (first entry)
 XX DE Human G-CSF gene enhancer region.
 XX DE CD28 signal transduction pathway; screening assay;
 KW CD-28-regulated nuclear binding protein responsive; ss.
 XX OS Homo sapiens.

PN WO9325712-A1.
XX 23-DEC-1993.
PD 11-JUN-1993; 93WO-US005668.
PF 15-JUN-1992; 92US-00898639.
PR (REGC) UNIV CALIFORNIA.
PA Weiss A, Fraser J;
PI WPI; 1994-007567/01.
DR Screening assay for identification of immunosuppressive drugs - by
PT ability to inhibit CD28 signal transduction pathway in T-cells.
PT Disclosure; Page 5; 18pp; English.
PS
XX The sequence is that of the enhancer region derived from the human G-CSF
CC gene which is responsive to a CD28-regulated nuclear binding protein.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 BP; 4 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGACTCGCTG 12
DB 11 TGGAACTCTG 1
RESULT 223
AAH26942/c
ID AAH26942 standard; DNA; 11 BP.
AC AAH26942;
XX
DT 11-SEP-2003 (revised)
DT 21-DEC-2001 (first entry)
XX Trichoderma reesei bipl promoter unfolded protein response element.
DE Unfolded protein response; bipl promoter; protein secretion; ss.
KW Hypocrea jecorina.
OS WO200172783-A2.
PN 04-OCT-2001.
XX 23-MAR-2001; 2001WO-US009401.
XX 24-MAR-2000; 2000US-00534692.
PR (GEWV) GENENCOR INT INC.
PA Penttila ME, Ward M, Wang H, Valkonen MJ, Saloheimo MLA;
PI WPI; 2001-626252/72.
DR Increasing secretion of heterologous proteins e.g. lipase and cellulase
PT in eukaryotic cells useful in industry to increase production and
PT facilitate purification, by inducing an elevated unfolded protein
PT response.
PS Example 6; Fig 16; 89pp; English.
XX The present sequence is that of an unfolded protein response (UPR)
CC element found in the bipl promoter of Trichoderma reesei. The element was
CC identified in bandshift experiments using a fusion protein composed of a

CC portion of T. reesei HAC1 protein (see AAB82975) fused to the Escherichia
CC coli maltose-binding protein male. The invention provides methods for
CC increasing the secretion of a heterologous protein in a cell by inducing
CC an elevated UPR. This can be achieved by modulating the activity of HAC1,
CC pT2 or IRE1 in the cell. The cell from which the protein is secreted can
CC be any cell having an UPR, such as mammalian cells, insect cells, yeast
CC and filamentous fungi. The protein of interest can be any secreted
CC protein such as a therapeutic protein or an industrial enzyme. (Updated
CC on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACTCGCTGCG 14
DB 11 GACACGTGGC 1
RESULT 224
AAF31235/c
ID AAF31235 standard; DNA; 11 BP.
XX
AC AAF31235;
XX
DT 09-APR-2001 (first entry)
XX
DE Novel BAC vector construction restriction site #4.
XX BAC vector; copy number; cloning; gene expression; pTRANS; pTRANS-SacB;
KW pBactA.PUC2; ds.
XX Synthetic.
OS
XX WO200078977-A1.
PN 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US016767.
XX
PR 18-JUN-1999; 99US-0140287P.
XX (AVET) AVENTIS PHARM INC.
PA Grossman T, Macneil I, August P;
PI WPI; 2001-102727/11.
DR Novel vector for increasing copy number and gene expression in plasmids,
PT comprises transposable element containing high copy number origin of
PT replication capable of in vitro transposition into target plasmid.
XX Disclosure; Fig 7; 40pp; English.
XX The present invention describes a vector for increasing the copy number
CC of plasmids, comprising a transposable element containing a high copy
CC number origin of replication capable of transposition into a target
CC plasmid. The vector may be pTRANS-SacB, pTRANS or pBactA.PUC2. The vector
CC can be used to facilitate the cloning of large inserts into BAC plasmids,
CC including full-length genes, the isolation of large amounts of BAC DNA
CC and the increased expression of BAC genes. They can also be used to
CC generate shuttle vectors without cloning
XX
SQ Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACTCGCTGCG 14
DB 11 GACACGTGGC 1

```

Db      11 GACTCTCTGTC 1

RESULT 225
ABQ86569
ID   ABQ86569 standard; cDNA; 11 BP.
XX
XX   ABQ86569;
XX
XX   10-SEP-2002 (first entry)
XX
XX   Human skin stress/ageing related EST SEQ ID NO 324.
XX
XX   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX   Homo sapiens.
XX
XX   WO200253773-A2.
XX
XX   11-JUL-2002.
XX
XX   20-DEC-2001; 2001WO-EP015178.
XX
XX   03-JAN-2001; 2001DE-01000121.
XX   (HENK ) HENKEL KGAA.
XX
XX   Petersohn D, Conradt M, Hofmann K;
XX
XX   WPI; 2002-528865/56.
XX
XX   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
XX   Claim 8; Page 50; 325pp; German.
XX
XX   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87650) of the invention
XX
XX   Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX   Query Match      39.0%; Score 7.8; DB 1; Length 11;
XX   Best Local Similarity 81.8%; Pred. No. 1.4e+02;
XX   Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      2 TGGACTCGCTG 12
        ||| ||| |||
DB      1 TGGCCTCTCTG 11

RESULT 226
ABQ87588
ID   ABQ87588 standard; cDNA; 11 BP.
XX
XX   ABQ87588;
XX
XX   10-SEP-2002 (first entry)
XX
XX   Human skin stress/ageing related EST SEQ ID NO 1343.
XX
XX   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX   Homo sapiens.

```

XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 154; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TGGACTCGCTG 12
DB 11 TGGAAATCACTG 1
XX
RESULT 228
ABV67072/c
ID ABV67072 standard; cDNA; 11 BP.
XX
AC ABV67072;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4858.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 285; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX

CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 10 CTGGCAGCAGC 20
DB 11 CTGGCAGCAGC 1
XX
RESULT 229
ABV71082/c
ID ABV71082 standard; cDNA; 11 BP.
XX
AC ABV71082;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8868.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 285; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX


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QY      9 GCTGGCAGCA 19
Db      11 GCTGGCAGCA 1
        |||||
RESULT 230
ABV63661/C
ID      ABV63661 standard; cDNA; 11 BP.
XX
AC      ABV63661;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 1447.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
FN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
DR      WPI; 2002-590638/63.
XX
PT      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Disclosure; Page 65; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
Query Match      39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      9 GCTGGCAGCA 19
Db      11 GCTGGCAGCA 1
        |||||
RESULT 231
ABV70367
ID      ABV70367 standard; cDNA; 11 BP.
XX
AC      ABV70367;
XX
DT      21-OCT-2002 (first entry)
XX
DE
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
FN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR
XX
PA
XX
PI
XX
DR
XX
PT
XX
PS
XX
CC
XX
SQ
XX
Query Match      39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      6 CTCGCTGCAC 16
Db      1 CTCACAGGCAC 11
        |||||
RESULT 232
ABV62946
ID      ABV62946 standard; cDNA; 11 BP.
XX
AC      ABV62946;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 732.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
FN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX

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DE      Human skin EST 8153.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
FN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
DR      WPI; 2002-590638/63.
XX
PT      In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Claim 24; Page 260; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
XX
Query Match      39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      6 CTCGCTGCAC 16
Db      1 CTCACAGGCAC 11
        |||||
RESULT 232
ABV62946
ID      ABV62946 standard; cDNA; 11 BP.
XX
AC      ABV62946;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 732.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
FN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX

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XX PR 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 45; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAC 16
 |||||
 DB 1 CTCACAGGCAC 11
 |||||
 RESULT 233
 ABV65539
 ID ABV65539 standard; cDNA; 11 BP.
 AC ABV65539;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 3325.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

PS Disclosure; Page 117; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 GCTGCGCAGCA 19
 |||||
 DB 1 GGTGGCACTCA 11
 |||||
 RESULT 234
 ABV62748
 ID ABV62748 standard; cDNA; 11 BP.
 AC ABV62748;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 534.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 40; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag

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CC (EST) of the invention
XX Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
DB 1 GTCTCGCTGAC 11

RESULT 235
ABV68415
ID ABV68415 standard; cDNA; 11 BP.
XX
AC ABV68415;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6201.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cystostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 197; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
DB 1 GACAGGCTGCG 11

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RESULT 236
ABV63730/C
ID ABV63730 standard; cDNA; 11 BP.
XX
AC ABV63730;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1516.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cystostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 66; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 11 TGGTCTCGGTG 1

RESULT 237
ABV65289
ID ABV65289 standard; cDNA; 11 BP.
XX
AC ABV65289;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3075.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cystostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

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Petersohn D, Conradt M, Hofmann K;
WPI; 2002-590638/63.
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
Claim 24; Page 253; 1345pp; German.
The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACTCGCTGGC 14
| | | | | | | | | |
Db 1 GTCTCGCTGAC 11
RESULT 239
ABV71151/c
ID ID ABV71151 standard; cDNA; 11 BP.
XX ABV71151;
XX
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 8937.
XX
XX Human; skin; dermatological; vulnervary; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
XX Claim 24; Page 287; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12

Db 11 TGGTCTCGGTG 1

RESULT 240

AA024644/C
 ID AAD24644 standard; DNA; 11 BP.

XX AC AAD24644;

XX DT 29-AUG-2003 (revised)

XX DT 07-MAR-2002 (first entry)

XX DE Trichoderma reesei b1p1 promoter UPR element, b1pUPREI.

XX KW Heterologous protein secretion; unfolded protein response; UPR; lipase;
 XX KX cellulase; carboxylase; industry; purification; HAC1-male protein;
 XX KW b1p1 promoter; b1pUPREI; ds.

XX OS Hypocrea jecorina.

XX FN US2001034045-A1.

XX PD 25-OCT-2001.

XX PF 23-MAR-2001; 2001US-00816277.

XX PR 24-MAR-2000; 2000US-00534692.

XX PA (GENV) GENENCOR INT INC.

XX PI Penttila ME, Ward M, Wang H, Valkonen MJ, Saloheimo MLA;

XX PI WPI; 2002-033728/04.

XX PT Increasing secretion of heterologous proteins e.g. lipase and cellulase
 PT in eukaryotic cells useful in industry to increase production and
 PT facilitate purification, by inducing an elevated unfolded protein
 PT response.

XX PS Example 6; Fig 16; 56pp; English.

XX CC The present invention relates to methods for increasing the secretion of
 CC heterologous protein in eukaryotic cells by inducing an elevated unfolded
 CC protein response (UPR). The method involves inducing the elevated UPR by
 CC increasing the presence of proteins such as HAC1, HACA, PTC2 or IRE1 in
 CC cells. The method and sequences are useful for increasing the secretion
 CC of heterologous proteins (e.g. lipase, cellulase, carboxylase) in
 CC eukaryotic cells useful in industry to increase protein yields and to
 CC facilitate purification. The present DNA sequence is Trichoderma reesei
 CC b1p1 promoter UPR element, b1pUPREI which bind HAC1-male protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14

Db 11 GACACGTTGGC 1

RESULT 241

AAQ24024/C
 ID AAQ24024 standard; DNA; 12 BP.

XX AC AAQ24024;

XX DT 25-MAR-2003 (revised)

XX DT 21-SEP-1992 (first entry)

XX DE Herpesvirus inhibiting antisense oligonucleotide.

XX KW HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
 XX KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.

XX OS Synthetic.

XX FN WO9205284-A.

XX PD 02-APR-1992.

XX PF 18-SEP-1991; 91WO-US006646.

XX PR 21-SEP-1990; 90US-00586185.

XX PA (UTMA-) UNIV MARYLAND BALTIMORE.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Aurelian L, Tso P;

XX DR WPI; 1992-132145/16.

XX PT New anti-sense oligo:nucleotide(s) for inhibiting HSV - also used for
 XX diagnosis and for inhibiting HIV activation by herpes virus.

XX PS Claim 1; Page 38; 77pp; English.

XX CC The sequence is that of an antisense oligonucleotide which can be used
 CC for inhibiting growth or replication of herpesviruses. It corresponds to
 CC an antisense sequence of a herpesvirus site, pref. in a gene that is
 CC essential for synthesising nucleic acids e.g. the immediate early genes
 CC or Vmw65. It can be prep'd. by solid phase triester or phosphor- amide
 CC chemistry or by recombinant DNA techniques. It can be used for treating
 CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
 CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
 CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
 CC inhibition of herpesvirus growth or replication may indirectly forestall
 CC the progression of events from HIV exposure to the clinical manifestation
 CC of AIDS. It may also be useful in the detection, diagnosis and
 CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
 CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 12 BP; 1 A; 1 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CTGCACGCGAC 20

Db 12 CTCCACGCGAC 2

RESULT 242

AA763015

ID AA763015 standard; DNA; 12 BP.

XX AAT63015;
 AC
 XX
 DT 02-FEB-1998 (first entry)
 DE
 XX
 DE TNF-alpha mRNA series 1 (5' untranslated cap region) oligonucleotide 2.
 XX
 XX Tumour necrosis factor alpha; TNF-alpha; therapeutic agent;
 KW chimeric oligonucleotide library; antisense binding site;
 KW antisense compound; drug target validation; 5' untranslated cap region;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX WO9710332-A2.
 PN
 XX
 XX 20-MAR-1997.
 PD
 XX
 PF 13-SEP-1996; 96WO-GB002275.
 XX
 XX 14-SEP-1995; 95GB-00018864.
 PR
 XX (BRAX-) BRAX GENOMICS LTD.
 PA
 XX Schmidt G;
 PI
 XX WPI; 1997-202228/18.
 DR
 XX Chimeric oligo:nucleotide library - for use in identifying anti-sense
 PT binding sites in target messenger RNA.
 PT
 XX Example 2; Page 27; 44pp; English.
 PS
 XX Oligonucleotides of series 1, AAT63014-21, have specific anti-mRNA
 CC sequences to the 5' untranslated cap region of tumour necrosis factor
 CC (TNF)-alpha mRNA. These oligonucleotides are an example of a new chimeric
 CC oligonucleotide library, used to identify an antisense binding site in a
 CC target mRNA (in this case TNF-alpha). The library comprises a set of
 CC distinct chimeric oligonucleotides capable of hybridising to mRNA to form
 CC a duplex, the nucleotide sequences of which each have a common length of
 CC 7-20 bases. All of the nucleotides of the common length which are present
 CC as subsequences in the target mRNA are present in the library. Each
 CC nucleotide sequence comprises a recognition region recognisable by a
 CC duplex-cutting RNase, and a flanking region of chemically modified
 CC nucleotides which binds to the mRNA sufficiently tightly to stabilise the
 CC duplex for the RNase. Each oligonucleotide is protected against
 CC exonuclease attack. The libraries can be used to identify optimal
 CC effective antisense compounds against specific mRNA targets. The
 CC antisense compounds are useful as potential therapeutic agents, and as
 CC tools for drug target validation
 XX
 SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 GCTGGCAGCA 19
 |||||
 Db 2 GCTGCCAGCA 12
 RESULT 243
 AAV32266/c
 ID AAV32266 standard; DNA; 12 BP.
 XX
 XX AAV32266;
 AC
 XX 18-AUG-1998 (first entry)
 DT
 XX Random primed reverse transcription PCR primer 355.
 DE
 XX RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
 KW

KW differential gene expression; ss.
 XX
 OS Synthetic.
 XX
 PN WO9813521-A1.
 XX
 XX 02-APR-1998.
 PD
 XX 26-SEP-1997; 97WO-EP005290.
 PF
 XX 27-SEP-1996; 96GB-00020216.
 PR
 XX (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
 PA
 XX Consalez G, Fesce R;
 XX WPI; 1998-230725/20.
 FI
 XX
 DR
 XX Differential screening of gene expression by reverse transcription
 PT polymerase chain reaction - uses random priming with primers selected for
 PT high efficiency and selectivity by computer screening of database(s).
 XX
 XX Claim 9; Page 24; 37pp; English.
 PS
 XX The invention provides a method for the differential screening of gene
 CC expression by random primed reverse transcription PCR (RT-PCR). The
 CC primer sequences are generated by stimulating PCR reactions on non-
 CC redundant mammalian nucleotide sequence databank entries containing at
 CC least 1,000 bp of coding region. The primers selected, such as the
 CC present one, had to meet various criteria such as having an efficiency
 CC index between 2-10, having a selectivity index higher than 1, being 12 bp
 CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others
 CC in at least 5 of the 8 bases at the 3'-end. The invention claims the
 CC selected primers make it possible to use internally primed, PCR-based RNA
 CC fingerprinting for simple, exhaustive and systematic analysis of
 CC differential gene expression as an advantageous alternative to
 CC differential display. The method can also be useful for isolating new
 CC coding sequences and to compare known and new genes
 XX
 SQ Sequence 12 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 1 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GGACTCGCTGG 13
 |||||
 Db 11 GAACACGCTGG 1
 |||||
 RESULT 244
 AAZ41820
 ID AAZ41820 standard; DNA; 12 BP.
 XX
 XX AAZ41820;
 AC
 XX 20-MAR-2003 (revised)
 DT 21-JAN-2000 (first entry)
 XX
 XX Organic material detecting primer 181.
 DE
 XX Amplification; polymerase chain reaction; PCR; microorganism; compost;
 KW detection; pollutant; soil; food; agricultural chemical; polymer;
 KW organochlorine; primer; ss.
 XX
 OS Synthetic.
 XX
 XX DE19914461-A1.
 PN
 XX 21-OCT-1999.
 PD
 XX 30-MAR-1999; 99DE-01014461.
 PF
 XX

```

PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
PA (NOR ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
XX Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
PS Example 1; Page 22; 78pp; German.
XX
XX This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-741855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 ACTCGCTGGCA 15
DB 1 ACTGGCGCGCA 11

RESULT 245
AAZ41604
ID AAZ41604 standard; DNA; 12 BP.
XX
XX AAZ41604;
XX
DT 19-JAN-2000 (first entry)
DE Microbe detection in organic waste arbitrarily primed PCR primer #181.
XX
XX Microbe; detection; organic waste; arbitrarily primer PCR;
XX random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
XX Synthetic.
XX
XX JF11276176-A.
XX
XX 12-OCT-1999.
XX
XX 31-MAR-1998; 98JP-00087652.
XX
XX 31-MAR-1998; 98JP-00087652.
XX
XX (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) 2H NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
XX WPI; 1999-626940/54.
XX
XX Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
XX
XX Example; Page 10; 40pp; Japanese.
XX

CC A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC organic waste
XX
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 ACTCGCTGGCA 15
DB 1 ACTGGCGCGCA 11

RESULT 246
AAZ55919
ID AAZ55919 standard; DNA; 12 BP.
XX
XX AAZ55919;
XX
DT 04-SEP-2000 (first entry)
DE Adapter linker nucleotide sequence SEQ ID NO:78.
XX
XX Yeast; detection; protein-protein interaction; DNA-binding domain;
XX characterisation; identification; protein pathway information;
XX protein interaction domain; screening; PCR primer; adapter; linker;
XX fusion protein; inhibitor; regulation; ss.
XX
XX Synthetic.
XX
XX US6057101-A.
XX
XX 02-MAY-2000.
XX
XX 13-JUN-1997; 97US-00874825.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;
XX
XX WPI; 2000-349567/30.
XX
XX Identifying, comparing and detecting inhibitors of protein-protein
XX interactions within population of host cells, involves detecting
XX regulation of transcription of nucleic acid sequence by fusion protein
XX interaction.
XX
XX Example; Col 131; 161pp; English.
XX
XX The present invention describes a method for detecting (D) at least 1
XX protein-protein interaction (PPI) by recombinantly expressing within a
XX population of host cells, populations of first and second fusion proteins
XX comprising DNA binding domain (DBD) and transcriptional regulatory domain
XX (TRD) respectively and detecting the regulation of transcription of
XX nucleotide sequence of host cells operably linked to a promoter driven by
XX DBD. The detection method (D) is useful for identifying inhibitors of PPI
XX for therapeutic use, and for detecting specific cell types, tissue types,
XX stage of development and disease states. From the population of the
XX proteins characteristic of the particular tissue or a cell-type, all
XX possible detectable PPI that occur can be identified and genes encoding
XX these proteins can be isolated. Thus, parallel analysis of two cell types
XX enumerates PPI that are common to both and those that are specific to
XX both. This analysis has significant value since PPI specific to a disease

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CC state can serve as therapeutic points of intervention. Inhibitors of PPI
 CC can also be isolated in rapid fashion. The number of false positives and
 CC low throughput are reduced. AAA55843 to AAA55963 and AY90961 are
 CC sequences used in the exemplification of the present invention

XX Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
 DB 1 TCGAGTCGCTG 11

RESULT 247

AAA55920
 ID AAA55920 standard; DNA; 12 BP.

XX AC AAA55920;

XX DT 04-SEP-2000 (first entry)

XX DE Adapter linker nucleotide sequence SEQ ID NO:79.

XX Yeast; detection; protein-protein interaction; DNA-binding domain;
 KW characterisation; identification; protein pathway information;
 KW protein interaction domain; screening; PCR primer; adapter; linker;
 KW fusion protein; inhibitor; regulation; ss.

XX OS Synthetic.

XX PN US6057101-A.

XX PD 02-MAY-2000.

XX PF 13-JUN-1997; 97US-00874825.

XX PR 14-JUN-1996; 96US-00663824.

XX PA (CURA-) CURAGEN CORP.

XX PI Knight JR, Kalbfleisch TS, Yang M, Mandabalan K, Rothberg JM;

XX DR WPI; 2000-349567/30.

XX Identifying, comparing and detecting inhibitors of protein-protein
 PT interactions within population of host cells, involves detecting
 PT regulation of transcription of nucleic acid sequence by fusion protein
 PT interaction.

XX Example; Col 131; 161pp; English.

XX The present invention describes a method for detecting (D) at least 1
 CC protein-protein interaction (PPI) by recombinantly expressing within a
 CC population of host cells, populations of first and second fusion proteins
 CC comprising DNA binding domain (DBD) and transcriptional regulatory domain
 CC (TRD) respectively and detecting the regulation of transcription of
 CC nucleotide sequence of host cells operably linked to a promoter driven by
 CC DBD. The detection method (D) is useful for identifying inhibitors of PPI
 CC for therapeutic use, and for detecting specific cell types, tissue types,
 CC stage of development and disease states. From the population of the
 CC proteins characteristic of the particular tissue or a cell-type, all
 CC possible detectable PPI that occur can be identified and genes encoding
 CC these proteins can be isolated. Thus, parallel analysis of two cell types
 CC enumerates PPI that are common to both and those that are specific to
 CC both. This analysis has significant value since PPI specific to a disease
 CC state can serve as therapeutic points of intervention. Inhibitors of PPI
 CC can also be isolated in rapid fashion. The number of false positives and
 CC low throughput are reduced. AAA55843 to AAA55963 and AY90961 are
 CC sequences used in the exemplification of the present invention

SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
 DB 1 TCGAGTCGCTG 11

RESULT 248

AAA92134/c
 ID AAA92134 standard; DNA; 12 BP.

XX AC AAA92134;

XX DT 04-JAN-2001 (first entry)

XX DE Human Lhx3 exon-intron boundary oligonucleotide #4.

XX Lhx3; LIM-3; P-LIM; identification; characterisation; diagnosis;
 KW chromosome 9; pituitary disease; subtelomeric region; mutation;
 KW pituitary trophic hormone gene promoter; ds.

XX OS Homo sapiens.

XX PN WO200050868-A2.

XX PD 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-US004424.

XX PR 22-FEB-1999; 99US-0121110P.

XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX PI Rhodes SJ, Bridwell JL, Meier BC, Parker GE, Price JR;

XX DR WPI; 2000-594085/56.

XX New isolated nucleic acid encoding mammalian Lhx3 for identifying a human
 PT with a disease, disorder, or condition caused by an altered level of
 PT expression or binding of Lhx3.

XX Example 5; Page 165; 239pp; English.

XX The present invention describes an isolated nucleic acid (I) encoding a
 CC mammalian Lhx3. (I) is used in assays to: (1) detect and quantify the
 CC presence and level of expression of Lhx3, Lhx3a or Lhx3b, in a sample;
 CC (2) identify a compound that affects expression, the level of expression,
 CC or the activity of Lhx3, Lhx3a, or Lhx3b in a cell; (3) identify a
 CC compound that affects binding of Lhx3 to nucleic acid or Lhx3 induction
 CC of a pituitary trophic hormone gene promoter; (4) identify a human
 CC afflicted with a disease, disorder, or condition caused by altered
 CC expression of Lhx3 or altered level of binding of Lhx3 to a nucleic acid;
 CC and (5) detect a mutation in a Lhx3 allele in a human. The coding region
 CC of human Lhx3 has been genomically mapped to the subtelomeric region of
 CC chromosome 9. Lhx3 is also known as P-LIM or LIM-3. The present sequence
 CC represents a human Lhx3 exon-intron boundary oligonucleotide, which is
 CC given in an example from the present invention

SQ Sequence 12 BP; 3 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
 DB 1 TCGAGTCGCTG 11


```

RESULT 249
AAA73431
ID AAA73431 standard; DNA; 12 BP.
XX
AC AAA73431;
XX
DT 09-FEB-2001 (first entry)
XX
DE Linker RC14.
XX
KW Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW ss.
XX
OS Saccharomyces cerevisiae.
XX
PN US6083693-A.
XX
PD 04-JUL-2000.
XX
PF 14-JUN-1996; 96US-00663824.
XX
PR 14-JUN-1996; 96US-00663824.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Nandabalan K, Rothberg JM;
XX
WPI; 2000-464335/40.
XX
PF 14-JUN-1996; 96US-00663824.
XX
PR 14-JUN-1996; 96US-00663824.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Nandabalan K, Rothberg JM;
XX
WPI; 2000-464335/40.
XX
DT Detecting protein-protein interactions in protein populations useful for
PT identifying genes encoding the proteins, and inhibitors of the
PT interactions, by detecting transcriptional regulation leading to reporter
PT gene activation.
XX
PF Example; Col 103-104; 135pp; English.
XX
CC The present invention relates to methods for detecting and isolating
CC genes encoding proteins that interact with each other, via the
CC reconstitution of a transcription factor and hence reporter gene
CC activation. Proteins are fused to either the yeast DNA-binding domain of
CC a transcriptional activator or to the activation domain of a
CC transcriptional activator. The present sequence is a linker used in the
CC present invention as an adapter in the analysis of yeast fusion genes.
CC The present method may be used to identify protein-protein interactions
CC and genes encoding the interacting proteins relevant to a particular
CC tissue, stage or disease e.g. cancer
XX
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
CC The present invention relates to methods for detecting and isolating
CC genes encoding proteins that interact with each other, via the
CC reconstitution of a transcription factor and hence reporter gene
CC activation. Proteins are fused to either the yeast DNA-binding domain of
CC a transcriptional activator or to the activation domain of a
CC transcriptional activator. The present sequence is a linker used in the
CC present invention as an adapter in the analysis of yeast fusion genes.
CC The present method may be used to identify protein-protein interactions
CC and genes encoding the interacting proteins relevant to a particular
CC tissue, stage or disease e.g. cancer
XX
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TGGACTCGCTG 12
DB 1 TCGAGTCGCTG 11
XX
RESULT 250
AAA73432
ID AAA73432 standard; DNA; 12 BP.
XX
AC AAA73432;
XX
DT 09-FEB-2001 (first entry)
XX
DE Linker RC15.
XX
KW Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW ss.
XX
OS Saccharomyces cerevisiae.

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```

XX
PN US6083693-A.
XX
PD 04-JUL-2000.
XX
PF 14-JUN-1996; 96US-00663824.
XX
PR 14-JUN-1996; 96US-00663824.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Nandabalan K, Rothberg JM;
XX
WPI; 2000-464335/40.
XX
DT Detecting protein-protein interactions in protein populations useful for
PT identifying genes encoding the proteins, and inhibitors of the
PT interactions, by detecting transcriptional regulation leading to reporter
PT gene activation.
XX
PF Example; Col 103-104; 135pp; English.
XX
CC The present invention relates to methods for detecting and isolating
CC genes encoding proteins that interact with each other, via the
CC reconstitution of a transcription factor and hence reporter gene
CC activation. Proteins are fused to either the yeast DNA-binding domain of
CC a transcriptional activator or to the activation domain of a
CC transcriptional activator. The present sequence is a linker used in the
CC present invention as an adapter in the analysis of yeast fusion genes.
CC The present method may be used to identify protein-protein interactions
CC and genes encoding the interacting proteins relevant to a particular
CC tissue, stage or disease e.g. cancer
XX
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TGGACTCGCTG 12
DB 1 TCGAGTCGCTG 11
XX
RESULT 251
AAC97955
ID AAC97955 standard; DNA; 12 BP.
XX
AC AAC97955;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 181.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
EN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NCRI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
WPI; 2001-011047/02.
XX
PT Amplification of a DNA fragment and its apparatus.
XX

```

PS Example 1; Page 11; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the
XX invention
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCA 15
DB 1 ACTGGCCGCA 11

RESULT 252
AAH79169
ID AAH79169 standard; DNA; 12 BP.
XX
AC AAH79169;
XX
DT 04-DEC-2001 (first entry)
XX
DE Oligonucleotide ODN I.
XX
KW Modified base; vinyl group; reversible ligation; irradiation;
KW gene therapy; DNA computing; immobilisation; ss.
XX
OS Synthetic.
XX
PN WO200166556-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-JP001670.
XX
PR 10-MAR-2000; 2000JP-00067519.
PR 05-JAN-2001; 2001JP-00000750.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Saito I, Fujimoto K, Matsuda S, Yoshino H;
DR WPI; 2001-589925/66.
XX
PT Nucleic acids and methods for reversible ligation using light
PT irradiation.
XX
PS Example 9; Page 30; 54pp; Japanese.
XX
CC The invention relates to nucleic acids containing a modified base,
CC especially a substituted vinyl group at the 5-position of a pyrimidine,
CC such that nucleic acids can be reversibly ligated to each other by light-
CC irradiation. The nucleic acids with unique structures can be synthesised
CC for use in gene therapy, DNA computing and immobilisation of nucleic
CC acids. The ligation and immobilisation processes involve the use of
CC light, which is environmentally friendly. The present sequence is that of
CC an oligonucleotide useful to the invention
XX
SQ Sequence 12 BP; 4 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAC 16
DB 1 CACGAGGCAC 11

RESULT 253
AAH79164
ID AAH79164 standard; DNA; 12 BP.
XX
AC AAH79164;
XX
DT 04-DEC-2001 (first entry)
XX
DE Oligonucleotide ODN C.
XX
KW Modified base; vinyl group; reversible ligation; irradiation;
KW gene therapy; DNA computing; immobilisation; ss.
XX
OS Synthetic.
XX
PN WO200166556-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-JP001670.
XX
PR 10-MAR-2000; 2000JP-00067519.
PR 05-JAN-2001; 2001JP-00000750.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Saito I, Fujimoto K, Matsuda S, Yoshino H;
DR WPI; 2001-589925/66.
XX
PT Nucleic acids and methods for reversible ligation using light
PT irradiation.
XX
PS Example 6; Page 28; 54pp; Japanese.
XX
CC The invention relates to nucleic acids containing a modified base,
CC especially a substituted vinyl group at the 5-position of a pyrimidine,
CC such that nucleic acids can be reversibly ligated to each other by light-
CC irradiation. The nucleic acids with unique structures can be synthesised
CC for use in gene therapy, DNA computing and immobilisation of nucleic
CC acids. The ligation and immobilisation processes involve the use of
CC light, which is environmentally friendly. The present sequence is that of
CC an oligonucleotide useful to the invention
XX
SQ Sequence 12 BP; 4 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAC 16
DB 1 CACGAGGCAC 11

RESULT 254
AAF56190
ID AAF56190 standard; DNA; 12 BP.
XX
AC AAF56190;
XX
DT 19-APR-2001 (first entry)
XX
DE Microarray capture probe k6.

XX Array-based nucleic acid hybridisation; hybridisation probe;
 KW microarray capture probe; ss.

XX Unidentified.

XX WO200106011-A2.

XX 25-JAN-2001.

XX 12-JUL-2000; 2000WO-US019045.

XX 14-JUL-1999; 99US-0143926P.

XX (GENO-) GENOMETRIX GENOMICS INC.

XX Belosludtsev Y;

XX WPI; 2001-147356/15.

XX Producing nucleic acid array for use in hybridization reactions, by
 PT employing adsorptive, non-covalent attachment of nucleic acids and
 PT oligonucleotide probes to positively charged solid surfaces.

XX Example 1; Page 29; 46pp; English.

XX The present sequence is a probe used to demonstrate array-based nucleic
 CC acid hybridisation. This was an example in a specification relating to a
 CC method for producing an array of discrete biosites comprising non-
 CC covalently attached nucleic acids. The nucleic acids are useful as probes
 CC in hybridisation reactions. The affinity and selectivity of the non-
 CC covalently immobilised probe to sample target duplex formation is
 CC excellent and compact compared to conventional methods and unlabelled
 CC probes are applied at a concentration which is at least five times lower
 CC than required for conventional methods

XX Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 1.5e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14

DB 1 GACCTGCTGGC 11

RESULT 255

AAF56187 ID AAF56187 standard; DNA; 12 BP.

XX AAF56187;

XX 19-APR-2001 (first entry)

XX Microarray capture probe k3.

XX Array-based nucleic acid hybridisation; hybridisation probe;
 KW microarray capture probe; ss.

XX Unidentified.

XX WO200106011-A2.

XX 25-JAN-2001.

XX 12-JUL-2000; 2000WO-US019045.

XX 14-JUL-1999; 99US-0143926P.

XX (GENO-) GENOMETRIX GENOMICS INC.

XX Belosludtsev Y;

XX

WPI; 2001-147356/15.

XX Producing nucleic acid array for use in hybridization reactions, by
 PT employing adsorptive, non-covalent attachment of nucleic acids and
 PT oligonucleotide probes to positively charged solid surfaces.

XX Example 1; Page 29; 46pp; English.

XX The present sequence is a probe used to demonstrate array-based nucleic
 CC acid hybridisation. This was an example in a specification relating to a
 CC method for producing an array of discrete biosites comprising non-
 CC covalently attached nucleic acids. The nucleic acids are useful as probes
 CC in hybridisation reactions. The affinity and selectivity of the non-
 CC covalently immobilised probe to sample target duplex formation is
 CC excellent and compact compared to conventional methods and unlabelled
 CC probes are applied at a concentration which is at least five times lower
 CC than required for conventional methods

XX Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 1.5e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14

DB 1 GACTTGGTGGC 11

RESULT 255

AAI65968

ID AAI65968 standard; DNA; 12 BP.

XX AAI65968;

XX 15-JAN-2002 (first entry)

XX Synthetic k-ras codon 12 point mutant capture probe K3.

XX Hybridisation device; single base pair difference; diagnostic test;
 KW protein purification; nucleic acid purification; secondary structure;
 KW probe; ss; k-ras; codon 12.

XX Synthetic.

XX WO200166687-A1.

XX 13-SEP-2001.

XX 24-AUG-2000; 2000WO-US023438.

XX 09-MAR-2000; 2000US-00522240.

XX 10-AUG-2000; 2000US-00636268.

XX (GENO-) GENOMETRIX GENOMIX INC.

XX Hogan M, Powdrill T, Iverson B, Belosludtsev Y, Belosludtsev Y;

XX WPI; 2001-611328/70.

XX Association device for nucleic acid-based diagnostic test, isolation of
 PT nucleic acids, comprises oligonucleotide probe and solid substrate having
 PT support surface comprising association surface for linking probe to
 PT substrate.

XX Example 13; Page 63; 101pp; English.

XX The invention relates to an association/hybridisation device comprising
 CC nucleic acid and polypeptide probes, or combinations of these, linked to
 CC a porous solid substrate, comprising an external substrate surface and
 CC several internal pores. The pore surfaces comprise an association surface
 CC which is charged with net positive or negative charge density where the

CC pH is lower or higher than the pI of association surface. The device is
 CC useful for associating a nucleic acid or a polypeptide in a sample to a
 CC nucleic acid or a polypeptide probe. The device is also useful for
 CC detecting a single base pair difference between a nucleic acid in a test
 CC sample and an oligonucleotide probe. The device finds application in
 CC nucleic acid-based diagnostic tests, isolation and purification of
 CC nucleic acids or polypeptides from a sample. The device can be used at
 CC any temperature and the kinetics of association between the
 CC oligonucleotide probe and the nucleic acid in the test sample are 10 fold
 CC more rapid than the kinetics of association under conditions when the
 CC substrate surface or association surface has a neutral or net negative
 CC charge density. The device and the method can be used for hybridisation
 CC of probes to target DNA or RNA at low bulk ion concentrations. The
 CC present sequence is that of a k-ras capture probe. As a representative
 CC DNA hybridisation model a 157bp PCR fragment of the human k-ras oncogene
 CC was used to examine hybridisation rate enhancement under low ionic
 CC strength and low pH conditions. The capture probes (AAI65972)
 CC comprise biologically significant codon 12 point mutations
 XX

CC Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. NO. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
 |||||
 Db 1 GACTTGGTGGC 11

RESULT 257
 AAI65971
 ID AAI65971 standard; DNA; 12 BP.
 XX
 AC AAI65971;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Synthetic k-ras codon 12 point mutant capture probe K6.
 XX
 KW Hybridisation device; single base pair difference; diagnostic test;
 KW protein purification; nucleic acid purification; secondary structure;
 KW probe; ss; k-ras; codon 12.
 XX
 OS Synthetic.
 XX
 PN WO200166587-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 24-AUG-2000; 2000WO-US023438.
 XX
 PR 09-MAR-2000; 2000US-00522240.
 PR 10-AUG-2000; 2000US-00636268.
 XX
 PA (GENO-) GENOMETRIX GENOMIX INC.
 XX
 PI Hogan M, Powdrill T, Iverson B, Belosludtsev YY, Belosludtsev IY;
 XX
 DR WPI; 2001-611328/70.
 XX
 XX Association device for nucleic acid-based diagnostic test, isolation of
 PT nucleic acids, comprises oligonucleotide probe and solid substrate having
 PT support surface comprising association surface for linking probe to
 PT substrate.
 XX

PS Example 13; Page 63; 101pp; English.
 XX
 CC The invention relates to an association/hybridisation device comprising
 CC nucleic acid and polypeptide probes, or combinations of these, linked to
 CC a porous solid substrate, comprising an external substrate surface and
 CC several internal pores. The pore surfaces comprise an association surface
 CC which is charged with net positive or negative charge density where the

CC pH is lower or higher than the pI of association surface. The device is
 CC useful for associating a nucleic acid or a polypeptide in a sample to a
 CC nucleic acid or a polypeptide probe. The device is also useful for
 CC detecting a single base pair difference between a nucleic acid in a test
 CC sample and an oligonucleotide probe. The device finds application in
 CC nucleic acid-based diagnostic tests, isolation and purification of
 CC nucleic acids or polypeptides from a sample. The device can be used at
 CC any temperature and the kinetics of association between the
 CC oligonucleotide probe and the nucleic acid in the test sample are 10 fold
 CC more rapid than the kinetics of association under conditions when the
 CC substrate surface or association surface has a neutral or net negative
 CC charge density. The device and the method can be used for hybridisation
 CC of probes to target DNA or RNA at low bulk ion concentrations. The
 CC present sequence is that of a k-ras capture probe. As a representative
 CC DNA hybridisation model a 157bp PCR fragment of the human k-ras oncogene
 CC was used to examine hybridisation rate enhancement under low ionic
 CC strength and low pH conditions. The capture probes (AAI65966-AAI65972)
 CC comprise biologically significant codon 12 point mutations
 XX

CC Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. NO. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
 |||||
 Db 1 GACTTGGTGGC 11

RESULT 258
 ABH83492
 ID ABH83492 standard; DNA; 12 BP.
 XX
 AC ABH83492;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 283485 for detecting SNP TSC0011339.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPICENOMICS AG.
 XX
 PI Olek A, Pispembrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 283485; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCT 11
    ||||| |||
Db 2 ATGGATTGGT 12
    ||||| |||

RESULT 259
ABH91416/c
ID ABH91416 standard; DNA; 12 BP.
XX AC ABH91416;
XX ABH91416;
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 291409 for detecting SNP TSC0014784.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 291409; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
    ||||| |||

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Db 12 TGGAGTCGATG 2
    ||||| |||
RESULT 260
ABH10618/c
ID ABH10618 standard; DNA; 12 BP.
XX AC ABH10618;
XX ABH10618;
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 310591 for detecting SNP TSC0024024.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 310591; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match          39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 18
    ||||| |||
Db 11 CGCGCGCAGC 1
    ||||| |||

RESULT 261
ABH85734
ID ABH85734 standard; DNA; 12 BP.
XX AC ABH85734;
XX ABH85734;
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 285727 for detecting SNP TSC0012410.

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XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 285727; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
CC
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACTCGCTGGC 14
DB 2 GACGCGTGCG 12
RESULT 262
ABH86519/C
ID ABH86519 standard; DNA; 12 BP.
XX ABH86519;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 286512 for detecting SNP TSC0012735.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX Oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 290180; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
CC
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACTCGCTGGC 14
DB 2 GACGCGTGCG 12
RESULT 263
ABH90187/C
ID ABH90187 standard; DNA; 12 BP.
XX ABH90187;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 290180 for detecting NP TSC0014238.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 290180; 29pp + Sequence Listing; German.

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PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 286512; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
CC
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CGCTGGCAGCG 18
DB 12 CGCGCGCAGCG 2
RESULT 263
ABH90187/C
ID ABH90187 standard; DNA; 12 BP.
XX ABH90187;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 290180 for detecting NP TSC0014238.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 290180; 29pp + Sequence Listing; German.

```

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 0 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CTGGCAGGCAC 20
Db 11 CCGCCAGGCAC 1
|||||

RESULT 264
ABH94001
ID ABH94001 standard; DNA; 12 BP.
AC ABH94001;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 293994 for detecting SNP TSC0015906.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 293994; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGGC 14
Db 1 GACTCGCTGGC 11
|||||

RESULT 265
ABI23556/c
ID ABI23556 standard; DNA; 12 BP.
AC ABI23556;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 323529 for detecting SNP TSC0031438.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 323529; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTGG 13
Db 12 GGACTCGCTGG 2
|||||

RESULT 266

ABI78918
ID ABI78918 standard; DNA; 12 BP.
XX AC ABI78918;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 378891 for detecting SNP TSC0062977.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 378891; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABIC2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABIC2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGACTCGCTG 12
DB 1 TGGACGCGTTG 11
RESULT 267
ABH74993/C
ID ABH74993 standard; DNA; 12 BP.
XX AC ABH74993;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 274980 for detecting SNP TSC0003748.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 274980; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABIC2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 TCGCTGGCAGC 17
DB 12 TCTCTCGCAGC 2
RESULT 268
ABH86581
ID ABH86581 standard; DNA; 12 BP.
XX AC ABH86581;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286574 for detecting SNP TSC0012735.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 286574; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABK00010-ABK99989
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 1 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 CGCTGCGACGC 18
 DB 1 CGCGGCGACGC 11
 RESULT 269
 AAS02759/c
 ID AAS02759 standard; DNA; 12 BP.
 XX
 AC AAS02759;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 XX Human pregnane X receptor (hPXR) gene, PCR primer #29.
 DE
 XX Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
 KW therapeutic; chemotherapy; gene therapy; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200120026-A2.
 PN
 XX 22-MAR-2001.
 PD
 XX 08-SEP-2000; 2000WO-EP008827.
 PF
 XX 10-SEP-1999; 99EP-00118120.
 PR
 XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 PA
 XX Wojnowski L, Hustert E;
 PI
 XX WPI; 2001-273428/28.
 DR
 XX Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 PT
 XX Claim 37; Page 39; 108pp; English.
 PS
 XX AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
 CC sequences and PCR primers of the invention. The human pregnane X receptor
 CC sequences are used to make antibodies, or a substance capable of binding
 CC specifically to the gene product of hPXR gene, for diagnosing and

CC treating various diseases, such as cancer, with drugs that are
 CC substrates, inhibitors or modulators of the hPXR gene product. The
 CC proteins can be used to identify and obtain produgs and drugs for
 CC treatment of diseases which are amenable to chemotherapy. The nucleic
 CC acids can be used in gene therapy for the treatment of prevention of
 CC disorders associated with hPXR expression
 XX
 XX Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 ACTCGCTGGCA 15
 DB 11 AGTCCCTGGCA 1
 RESULT 270
 AAI71695
 ID AAI71695 standard; DNA; 12 BP.
 XX
 AC AAI71695;
 XX
 XX 22-JAN-2002 (first entry)
 DT
 XX AAV containing growth hormone gene related inverted terminal repeat.
 DE
 XX AAV; adeno-associated virus; growth hormone gene; growth; GH; vector;
 KW inverted terminal repeat; ds.
 XX
 XX Unidentified.
 OS
 XX WO200175134-A1.
 PN
 XX 11-OCT-2001.
 PD
 XX 26-FEB-2001; 2001WO-CN000144.
 PF
 XX 24-FEB-2000; 2000CN-00103044.
 PR
 XX (DONG/) DONG X.
 PA
 XX Dong X, Zhang L;
 PI
 XX WPI; 2001-662976/76.
 DR
 XX Recombinant adeno-associated virus containing growth hormone gene or
 XX related genes, useful for accelerating swine growth and increasing lean
 XX meat ratio.
 PT
 XX Disclosure; Page 6; 26pp; Chinese.
 PS
 XX The present invention relates to a recombinant adeno-associated virus
 CC (AAV) which expresses a DNA comprising a growth hormone gene. This can be
 CC used to express growth hormone in a infected swine, which leads to
 CC increased growth and food conversion and improved meat quality. The
 CC present sequence is an inverted terminal repeat described in the
 CC exemplification of the invention
 CC
 XX Sequence 12 BP; 0 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CTCGCTGGCAC 16
 DB 2 CTCGCTGGCTC 12
 RESULT 271
 ABL91654/c

IDL ABL91654 standard; DNA; 12 BP.
 AC ABL91654;
 DT 29-JUL-2002 (first entry)
 XX
 DE SpeI 5' PCR primer tail used in Chlamydia pneumoniae gene amplification.
 XX
 XX Chlamydia pneumoniae; chlamydial infection; antigen; immunogen; vaccine;
 KW diagnosis; human respiratory disease; cardiovascular disease;
 KW atherosclerosis; coronary artery disease; carotid artery stenosis;
 KW myocardial infarction; cerebrovascular disease; aortic aneurysm;
 KW claudication; stroke; strain CWL029; open reading frame; ORF;
 KW Escherichia coli; recombinant expression; primer tail sequence; PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO200202606-A2.
 PN
 XX
 PD 10-JAN-2002.
 XX
 XX 03-JUL-2001; 2001WO-IB001445.
 XX
 XX 03-JUL-2000; 2000GB-00016363.
 PR
 PR 11-JUL-2000; 2000GB-00017047.
 PR
 PR 21-JUL-2000; 2000GB-00017983.
 PR
 PR 07-AUG-2000; 2000GB-00019368.
 PR
 PR 18-AUG-2000; 2000GB-00020440.
 PR
 PR 14-SEP-2000; 2000GB-00022583.
 PR
 PR 10-NOV-2000; 2000GB-00027549.
 PR
 PR 22-DEC-2000; 2000GB-00031706.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 XX Ratti G, Grandi G;
 PI
 XX
 XX WPI; 2002-154726/20.
 DR
 XX
 XX
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
 XX
 XX Example; Page 33; 364pp; English.
 XX
 CC Sequences AB90526-AB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL9184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. Sequences ABL91352-ABL91657 represent PCR
 CC primer tail sequences containing restriction enzyme sites used in the
 CC exemplifications in the amplification of the novel Chlamydia pneumoniae
 CC open reading frames (ORFs) for cloning into Escherichia coli expression
 CC vectors
 XX
 SQ Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 CTGCACGCAC 20
 ||| |||||

Db 11 CTAGTACGCAC 1
 RESULT 272
 AAD45523
 ID AAD45523 standard; DNA; 12 BP.
 XX
 XX AAD45523;
 AC
 XX 27-DEC-2002 (first entry)
 DT
 XX RC15 linker DNA used to illustrate the method of the invention.
 DE
 XX Protein-protein interaction; detection; cancer; linker; ss.
 KW
 XX Unidentified.
 OS
 XX US6410239-B1.
 PN
 XX 25-JUN-2002.
 PD
 XX 14-DEC-1999; 99US-00461125.
 XX
 XX 14-JUN-1996; 96US-00663824.
 PR
 PR 13-JUN-1997; 97US-00874825.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;
 PI
 XX WPI; 2002-654433/70.
 DR
 XX
 XX Detection of protein to protein interactions amongst two protein
 PT populations useful e.g. to identify interactions specific for particular
 PT tissues or diseases and to identify inhibitors of interactions uses a new
 PT genetic method.
 XX
 XX Example; Col 197; 152pp; English.
 PS
 XX
 CC The present invention relates to novel methods for detecting protein to
 CC protein interactions amongst two populations of proteins, each having a
 CC complexity of at least 100. The method involves using new genetic methods
 CC in which encoded proteins are fused to either the DNA-binding domain of a
 CC transcriptional activator or the activation domain of a transcriptional
 CC activator. The methods are useful to detect interacting proteins and to
 CC identify protein-protein interactions specific for a particular species,
 CC tissue, stage of development or disease state, e.g. by comparing protein-
 CC protein interactions between populations from cDNA of cancerous or pre-
 CC cancerous cells with those from non-cancerous cells. They are also useful
 CC to identify inhibitors interfering with protein-protein interactions e.g.
 CC potential drug candidates inhibiting interactions specific to cancerous
 CC cells. The present sequence is a linker DNA used to illustrate the method
 CC of the invention
 XX
 SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGGACTCGCTG 12
 ||| |||||
 Db 1 TGCAGTCGCTG 11
 RESULT 273
 AAD45522
 ID AAD45522 standard; DNA; 12 BP.
 XX
 XX AAD45522;
 AC
 XX 27-DEC-2002 (first entry)
 DT
 XX

DE RC14 linker DNA used to illustrate the method of the invention.

KW Protein-protein interaction; detection; cancer; linker; ss.

XX Unidentified.

OS US6410239-B1.

PN 25-JUN-2002.

PD 14-DEC-1999; 99US-00461125.

PF 14-JUN-1996; 96US-00663824.

PR 13-JUN-1997; 97US-00874825.

XX (CURA-) CURAGEN CORP.

XX Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;

XX WPI; 2002-654433/70.

XX Detection of protein to protein interactions amongst two protein

PT populations useful e.g. to identify interactions specific for particular

PT tissues or diseases and to identify inhibitors of interactions uses a new

PT genetic method.

XX Example; Col 137; 152pp; English.

PS The present invention relates to novel methods for detecting protein to

XX protein interactions amongst two populations of proteins, each having a

CC complexity of at least 100. The method involves using new genetic methods

CC in which encoded proteins are fused to either the DNA-binding domain of a

CC transcriptional activator or the activation domain of a transcriptional

CC activator. The methods are useful to detect interacting proteins and to

CC identify protein-protein interactions specific for a particular species,

CC tissue, stage of development or disease state, e.g. by comparing protein-

CC protein interactions between populations from cDNA of cancerous or pre-

CC cancerous cells with those from non-cancerous cells. They are also useful

CC to identify inhibitors interfering with protein-protein interactions e.g.

CC potential drug candidates inhibiting interactions specific to cancerous

CC cells. The present invention is a linker DNA used to illustrate the method

XX of the invention

SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 1.5e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGGACTCGCTG 12

DB 1 TCGAGTCGCTG 11

RESULT 274

ABS68785

ID ABS68785 standard; DNA; 12 BP.

AC ABS68785;

XX 20-NOV-2002 (first entry)

DE INVADER-directed cleavage assay, probe #8.

XX Phosphoramidite; INVADER assay cleavage reaction; PEN1; cleavage;

KW nucleic acid separation; DNA polymerase; human; MCP-1; ubiquitin;

KW monocyte chemoattractant protein-1; PCR; primer; probe; ss.

XX Synthetic.

OS WO200263030-A2.

PN 15-AUG-2002.

XX

PD

XX

PF

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PR

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XX

06-FEB-2002; 2002WO-US003423.

06-FEB-2001; 2001US-00777430.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Lyamichev V, Skrzypczynski Z, Allawi HT, Wayland SR, Takova T;

Neri BP;

WPI; 2002-674850/72.

Composition useful for e.g. separation of nucleic acids comprises a

positively or neutrally charged phosphoramidite.

Example 9; Page 71; 197pp; English.

The invention relates to a composition comprising a positively or

neutrally charged phosphoramidite. The composition is useful for

separation of nucleic acid molecules. The composition is further useful

for fractionation of specific nucleic acids by selective charge reversal

useful in e.g. INVADER assay cleavage reactions; and in the synthesis of

charge-balanced molecules. In the fractionation of nucleic acid

molecules, the method provides an absolute readout of the partition of

products from substrates (i.e. provides a 100% separation). Through the

use of multiple positively charged adducts, synthetic molecules can be

constructed with sufficient modification due to the fact that the

normally negatively charged strand is made nearly neutral. It is also

possible to distinguish between an enzymatically or thermally degraded DNA

fragments due to the absence or presence of 3'phosphate. ABS68740-

CC ABS68813 represent coding sequences and primers used in the method of the

CC invention

SQ Sequence 12 BP; 0 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 39.0%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 1.5e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 CGCTGGCAGCC 18

DB 1 CGCTGCTCGC 11

RESULT 275

AAF91643/C

ID AAF91643 standard; DNA; 9 BP.

AC AAF91643;

XX 10-MAY-2001 (first entry)

DE Breast-cancer associated protein isoform BPI-46 preferred probe.

XX Human; breast cancer; breast cancer associated protein isoform; BPI;

KW breast cancer associated feature; BP; diagnosis; cytostatic; probe; ss.

XX Homo sapiens.

XX WO200113117-A2.

XX 22-FEB-2001.

PD 14-AUG-2000; 2000WO-GB003143.

XX 13-AUG-1999; 99GB-00019258.

PR 30-MAR-2000; 2000GB-00007754.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA Herath HMAAC;

XX WPI; 2001-211252/21.

XX Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
 PT of serum or plasma by two dimensional electrophoresis to detect the
 PT presence or level of a breast cancer-associated feature.
 XX
 PS Claim 132; Page 41; 146pp; English.
 XX
 CC The present invention describes a method for the screening, diagnosis or
 CC prognosis of breast cancer (BC), determining the stage or severity of BC,
 CC and monitoring the effect of therapy administered to a subject having BC,
 CC comprising analysing a sample of body fluid by two dimensional
 CC electrophoresis to generate a two-dimensional array of features,
 CC comprising a chosen feature whose abundance correlates with BC or
 CC predicts the onset or course of BC. The method (I) involves: (a)
 CC analysing a sample of body fluid from the subject by two-dimensional
 CC electrophoresis to generate a two-dimensional array of features,
 CC comprising a chosen feature whose relative abundance correlates with BC
 CC or predicts the onset of BC; and (b) comparing the abundance of each
 CC chosen feature in the sample with the abundance of that chosen feature in
 CC the body fluid from one or more persons free from BC, or with a
 CC previously determined reference range for that feature in subjects free
 CC from BC, or with the abundance of an expression reference feature (ERF)
 CC in the test sample. The method is useful for screening, diagnosis or
 CC prognosis of breast cancer, determining the stage or severity of BC,
 CC monitoring the effect of therapy administered to a subject having BC, and
 CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
 CC represents breast cancer associated protein isoform (BPI) peptide
 CC sequences, and AAB91643 to AAB91848 represent BPI probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1e+03;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCACGC 18
 |||||
 Db 9 CTGGCACTC 1

RESULT 276
 ABQ71989
 ID ABQ71989 standard; DNA; 9 BP.
 AC
 AC ABQ71989;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:2287.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX

(SANG-) SANGAMO BIOSCIENCES INC.

Liu Q;

WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 PT

XX Example 1; Page 59; 81pp; English.
 PS
 CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (i) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triple target subsites
 CC having the nucleotide G in the 5'-most position of the subsites. (I) is
 CC useful in studying gene function, and for human therapeutic methods to
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and AAB48191 to AAB51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1e+03;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
 |||||
 Db 1 ATGGACTTG 9

RESULT 277
 ABQ71918
 ID ABQ71918 standard; DNA; 9 BP.

XX
 AC ABQ71918;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:2216.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 PT

XX Example 1; Page 58; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such that
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I) (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
Db 1 ATGGACTTG 9

RESULT 278
ABQ71988
ID ABQ71988 standard; DNA; 9 BP.

XX AC ABQ71988;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2286.

DE Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 59; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide

CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I) (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX

SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
Db 1 ATGGACTTG 9

RESULT 279

ADA64315

ID ADA64315 standard; DNA; 9 BP.

XX AC ADA64315;

XX 20-NOV-2003 (first entry)

XX Zinc finger target sequence DNA #773.

XX ds; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.

XX Synthetic.

XX US2003068675-A1.

XX 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

XX 30-JUL-1999; 99US-0146595P.

XX 30-JUL-1999; 99US-0146615P.

XX 23-MAR-2000; 2000US-00535008.

XX 20-NOV-2000; 2000US-00716637.

XX (LIUQ) LIU Q.

XX Liu Q;

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 24; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9
|||||

RESULT 280
ADA64316
ID ADA64316 standard; DNA; 9 BP.
XX
AC ADA64316;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #774.
XX
ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
XX WPI; 2003-567233/53.
XX
DR Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 25; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9
|||||

RESULT 281
ADA64245
ID ADA64245 standard; DNA; 9 BP.
XX
AC ADA64245;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #703.
XX
ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
XX WPI; 2003-567233/53.
XX
DR Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
DB 1 ATGGACTTG 9
|||||

RESULT 282
AAQ97071
ID AAQ97071 standard; DNA; 10 BP.
XX
AC AAQ97071;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 LTR nucleotide deletion 53.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.

XX PD 17-AUG-1995.
 XX PF 14-FEB-1995; 95WO-AU0000063.
 XX PR 14-FEB-1994; 94AU-00003864.
 XX PR 21-FEB-1994; 94AU-00004002.
 XX PR 23-DEC-1994; 94AU-00000284.
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PA (AURE-) AUSTRALIAN RED CROSS SOC.
 XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
 XX WPI; 1995-293115/38.
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
 PT LTR region - can be used in a vaccine to inhibit/reduce productive
 PT infection in an individual by a pathogenic strain.
 XX Claim 14; Page 197; 301pp; English.
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
 CC more deanculeotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
 CC deanculeotides (AAQ97019-Q97166) from the LTR region; the sequence of
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
 CC resulting avirulent HIV strains are still capable of inducing an immune
 CC response in humans, and enable the generation of therapeutic, diagnostic
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CTCGCTGGC 14
 DB 1 CTCCTGGC 9
 RESULT 283
 AAQ97136/c
 ID AAQ97136 standard; DNA; 10 BP.
 XX AC AAQ97136;
 XX DT 16-OCT-2003 (revised)
 XX DT 27-MAR-1996 (first entry)
 XX DE HIV-1 NL4-3 LTR nucleotide deletion 118.
 XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
 XX OS Human immunodeficiency virus 1.
 XX PN WO9521912-A1.
 XX PD 17-AUG-1995.
 XX PF 14-FEB-1995; 95WO-AU0000063.
 XX PR 14-FEB-1994; 94AU-00003864.
 XX PR 21-FEB-1994; 94AU-00004002.
 XX PR 23-DEC-1994; 94AU-00000284.
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PA (AURE-) AUSTRALIAN RED CROSS SOC.
 XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
 XX WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
 PT LTR region - can be used in a vaccine to inhibit/reduce productive
 PT infection in an individual by a pathogenic strain.
 XX Claim 14; Page 197; 301pp; English.
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
 CC more deanculeotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
 CC deanculeotides (AAQ97019-Q97166) from the LTR region; the sequence of
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
 CC resulting avirulent HIV strains are still capable of inducing an immune
 CC response in humans, and enable the generation of therapeutic, diagnostic
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GGCACGCAC 20
 DB 10 GGCACACAC 2
 RESULT 284
 AAQ97137/c
 ID AAQ97137 standard; DNA; 10 BP.
 XX AC AAQ97137;
 XX DT 16-OCT-2003 (revised)
 XX DT 27-MAR-1996 (first entry)
 XX DE HIV-1 NL4-3 LTR nucleotide deletion 119.
 XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
 XX OS Human immunodeficiency virus 1.
 XX PN WO9521912-A1.
 XX PD 17-AUG-1995.
 XX PF 14-FEB-1995; 95WO-AU0000063.
 XX PR 14-FEB-1994; 94AU-00003864.
 XX PR 21-FEB-1994; 94AU-00004002.
 XX PR 23-DEC-1994; 94AU-00000284.
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PA (AURE-) AUSTRALIAN RED CROSS SOC.
 XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
 XX WPI; 1995-293115/38.
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
 PT LTR region - can be used in a vaccine to inhibit/reduce productive
 PT infection in an individual by a pathogenic strain.
 XX Claim 14; Page 197; 301pp; English.
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
 CC more deanculeotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
 CC deanculeotides (AAQ97019-Q97166) from the LTR region; the sequence of
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
 CC resulting avirulent HIV strains are still capable of inducing an immune
 CC response in humans, and enable the generation of therapeutic, diagnostic
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
 CC standardise OS field)

```

XX SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGAC 20
DB 9 GGCACACAC 1

RESULT 285
AAQ97070
ID AAQ97070 standard; DNA; 10 BP.
XX AC AAQ97070;
XX AC AAQ97070;
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 LTR nucleotide deletion 52.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NU, Learmont JC, Mephee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX PS Claim 14; Page 197; 301pp; English.
XX SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
DB 2 CTCCTCTGGC 10

RESULT 286
AAT28375
ID AAT28375 standard; DNA; 10 BP.
XX AC AAT28375;
XX DT 05-NOV-1986 (first entry)
XX DE DNA-PEG-maleimide.
XX KW Systemic evolution of ligands by exponential enrichment; SELEX; therapy;
KW random pool sequence; prophylactic; cosmetic; agricultural composition;
KW parallel SELEX; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 10
XX FT /*tag= a
XX FT /note= "PMOC-PEG-maleimide labelled"
XX PN WO9609316-A1.
XX PD 28-MAR-1996.
XX PF 19-SEP-1995; 95WO-US011982.
XX PR 20-SEP-1994; 94US-00309245.
XX PA (NEXS-) NEXSTAR PHARM INC.
XX PI Eaton B, Gold L;
XX DR WPI; 1996-188395/19.
XX FT Novel parallel SELEX method - uses nucleic acid-reactant mixture to
XX PT produce e.g. therapeutic, diagnostic and agricultural compsns.
XX PS Example 1; Page 51; 78pp; English.
XX CC AAT28375-T28379 represent oligonucleotides used in the method of the
XX CC invention. This sequence represents a DNA-PEG-maleimide sequence, which
XX CC was ligated to a random pool sequence (see AAT28376) using a DNA bridge
XX CC oligonucleotide (see AAT28377) to obtain a nucleic acid-reactant test
XX CC mixture. The conjugate is then reacted with a second reactant (a
XX CC biotinylated diene prepared from NHS-biotin and 2,4-hexadien-1-ol). The
XX CC products were loaded on an immobilised streptavidin column and the bound
XX CC RNA was released by treatment with proteinase K. The eluted RNA was then
XX CC reverse transcribed, amplified by PCR and the double stranded DNA
XX CC obtained transcribed as in typical systemic evolution of ligands by
XX CC exponential enrichment (SELEX) reactions. This process is repeated to
XX CC obtain the desired product. This method can be used to identify products
XX CC that bind to, or perform a preselected function on, a target sequence.
XX CC The products and the methods can be used to produce therapeutic,
XX CC diagnostic, prophylactic, cosmetic or agricultural compositions. This
XX CC parallel SELEX reaction comprises forming a product library by contacting
XX CC two or more reactants. The method does not require keeping track of a
XX CC matrix of products, and does not require highly efficient or rapid
XX CC reactions. Product formation is directed by nucleic acids which when
XX CC specifying a desirable product can be easily amplified and the product
XX CC can be reliably reproduced in subsequent rounds of production
XX SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
DB 2 CAGGCAGC 10

RESULT 287
AAV20692
ID AAV20692 standard; RNA; 10 BP.

```

```

XX AC AAT28375;
XX DT 05-NOV-1986 (first entry)
XX DE DNA-PEG-maleimide.
XX KW Systemic evolution of ligands by exponential enrichment; SELEX; therapy;
KW random pool sequence; prophylactic; cosmetic; agricultural composition;
KW parallel SELEX; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 10
XX FT /*tag= a
XX FT /note= "PMOC-PEG-maleimide labelled"
XX PN WO9609316-A1.
XX PD 28-MAR-1996.
XX PF 19-SEP-1995; 95WO-US011982.
XX PR 20-SEP-1994; 94US-00309245.
XX PA (NEXS-) NEXSTAR PHARM INC.
XX PI Eaton B, Gold L;
XX DR WPI; 1996-188395/19.
XX FT Novel parallel SELEX method - uses nucleic acid-reactant mixture to
XX PT produce e.g. therapeutic, diagnostic and agricultural compsns.
XX PS Example 1; Page 51; 78pp; English.
XX CC AAT28375-T28379 represent oligonucleotides used in the method of the
XX CC invention. This sequence represents a DNA-PEG-maleimide sequence, which
XX CC was ligated to a random pool sequence (see AAT28376) using a DNA bridge
XX CC oligonucleotide (see AAT28377) to obtain a nucleic acid-reactant test
XX CC mixture. The conjugate is then reacted with a second reactant (a
XX CC biotinylated diene prepared from NHS-biotin and 2,4-hexadien-1-ol). The
XX CC products were loaded on an immobilised streptavidin column and the bound
XX CC RNA was released by treatment with proteinase K. The eluted RNA was then
XX CC reverse transcribed, amplified by PCR and the double stranded DNA
XX CC obtained transcribed as in typical systemic evolution of ligands by
XX CC exponential enrichment (SELEX) reactions. This process is repeated to
XX CC obtain the desired product. This method can be used to identify products
XX CC that bind to, or perform a preselected function on, a target sequence.
XX CC The products and the methods can be used to produce therapeutic,
XX CC diagnostic, prophylactic, cosmetic or agricultural compositions. This
XX CC parallel SELEX reaction comprises forming a product library by contacting
XX CC two or more reactants. The method does not require keeping track of a
XX CC matrix of products, and does not require highly efficient or rapid
XX CC reactions. Product formation is directed by nucleic acids which when
XX CC specifying a desirable product can be easily amplified and the product
XX CC can be reliably reproduced in subsequent rounds of production
XX SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
DB 2 CAGGCAGC 10

RESULT 287
AAV20692
ID AAV20692 standard; RNA; 10 BP.

```



```

XX AAV20692;
XX
XX 24-JUN-1998 (first entry)
XX
XX TAR mimetic oligonucleotide SEQ ID NO:4.
XX
XX Human; placental alkaline phosphatase; PAP; gene expression; RNA;
XX human immunodeficiency virus; HIV; TAR; mimetic; ss.
XX
XX Unidentified.
XX
XX US5736294-A.
XX
XX 07-APR-1998.
XX
XX 27-JUN-1991; 91US-00724500.
XX
XX 21-MAR-1990; 90US-00497090.
XX 19-MAR-1991; 91WO-US001822.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bruce TW, Vickers TA, Ecker DJ;
XX
XX WPI; 1998-239195/21.
XX
XX Inhibition of HIV replication in vitro - comprises contacting virus with
XX RNA oligo:nucleotide or its analogue.
XX
XX Disclosure; Col 10; 27pp; English.
XX
XX The present sequence is shown in the disclosure of the present invention.
XX The present invention describes methods for interfering with HIV
XX replication in vitro comprising: (1) contacting the virus with an
XX oligonucleotide (ON) or its analogue comprising the sequence (I); (2)
XX contacting the virus with ON or its analogue comprising the sequence (II)
XX and (3) contacting the virus with ON or its analogue comprising 6-50 nt
XX and a sequence selected from the group consisting of (III), (IV) and (V):
XX 5'-CUGGA-3' (I) 5'-UCUGAGCCUGGAGCUC-3' (II) 5'-NNUCUNN-3' (III) 5'-
XX NNUNN-3' (IV) 5'-NNUNN-3' (V) N = not defined. The methods can be used
XX to provide compositions and therapies for human diseases, e.g. viral and
XX retroviral infections
XX
XX Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 37.0%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 66.7%; Pred. No. 1.6e+02;
XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 CTCGCTGGC 14
XX | : | : | : |
XX 2 CUCUCUGGC 10
XX
XX
XX RESULT 288
XX AAX01788
XX ID AAX01788 standard; DNA; 10 BP.
XX
XX AC AAX01788;
XX
XX 09-APR-1999 (first entry)
XX
XX 10mer oligonucleotide DNA.
XX
XX Product cosolution; function; target; therapy; prophylactic; diagnosis;
XX cosmetic; library; primer; ss.
XX
XX Synthetic.
XX
XX US5858660-A.
XX
XX 12-JAN-1999.
XX

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XX 20-MAR-1996; 96US-00618700.
XX
XX 20-SEP-1994; 94US-00309245.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Eaton B;
XX
XX WPI; 1999-119866/10.
XX
XX Production of a product having the ability to perform a preselected
XX function on a target - comprises preparing a nucleic acid test mixture,
XX coupling with a first reactant, forming a product library, contacting
XX with target, and partitioning the product.
XX
XX Example 4; Col 48; 51pp; English.
XX
XX This sequence is an oligonucleotide used in a method for coevolving
XX products from two or more reactants, along with the nucleic acid that can
XX facilitate the reaction for making the products. The product can have the
XX ability to perform a preselected function on a target. The process can be
XX used to produce products having various therapeutic, prophylactic,
XX diagnostic and cosmetic uses, such as pyridines. The process produces a
XX large, structurally diverse library of products
XX
XX Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 37.0%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 1.6e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 CTGGCAGC 18
XX | : | : | : |
XX 2 CAGGCAGC 10
XX
XX
XX RESULT 289
XX AAX05660
XX ID AAX05660 standard; RNA; 10 BP.
XX
XX AC AAX05660;
XX
XX 23-APR-1999 (first entry)
XX
XX HIV-1 TAR mimetic oligonucleotide loopless delTAR #2246.
XX
XX Human immunodeficiency virus; HIV; trans-acting responsive element;
XX gene expression; viral; retroviral; infection; AIDS; mimetic; TAR;
XX acquired immunodeficiency syndrome; ss.
XX
XX Synthetic.
XX
XX Human immunodeficiency virus 1.
XX
XX US5874564-A.
XX
XX 23-FEB-1999.
XX
XX 05-JUN-1995; 95US-00461418.
XX
XX 21-MAR-1990; 90US-00497090.
XX 19-MAR-1991; 91WO-US001822.
XX 16-SEP-1992; 92US-00927505.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Vickers T, Ecker DJ, Bruce TW;
XX
XX WPI; 1999-180068/15.
XX
XX New oligonucleotides for modulating gene expression by RNA mimicry -
XX useful for treating viral and retroviral diseases such as AIDS.
XX

```

PS Claim 14; Col 26; 22pp; English.

XX The invention relates to defined oligonucleotides (or their analogues)

CC that are able to mimic the secondary or tertiary structure of RNA

CC molecules, especially mRNA. It provides specific oligonucleotides

CC (AA05657-661) which mimic the human immunodeficiency virus (HIV) trans-

CC acting responsive element (TAR). The RNA mimicry oligonucleotides mimic

CC particular strands of RNA, especially mRNA, containing secondary

CC structures important for RNA/protein interactions. The interaction of

CC proteins with mimic molecules minimises the interactions of proteins with

CC regulatory RNA. The oligonucleotides are useful for regulating/ modifying

CC gene expression and can be used in therapeutics for the treatment of

CC viral and retroviral infections such as acquired immunodeficiency

CC syndrome (AIDS). The oligonucleotides are also useful as probes in

CC diagnostic and research reagents, and kits. The present sequence

CC represents a specifically claimed TAR mimetic oligo

XX

XX Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

XX

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14

Db 2 CUCUCUGGC 10

RESULT 290

AAZ78047/C

ID AAZ78047 standard; DNA; 10 BP.

XX

AC AAZ78047;

XX

XX 10-APR-2000 (first entry)

XX

DE Human dendritic cell SAGE tag, SEQ ID NO:475.

XX

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;

KW immunostimulatory cofactor; costimulatory factor; CTL;

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX

OS Homo sapiens.

XX

XX W09965924-A2.

XX

XX 23-DEC-1999.

XX

PF 18-JUN-1999; 99WO-US013800.

XX

PR 19-JUN-1998; 98US-0089933P.

PR 19-JUN-1998; 98US-0089944P.

PR 19-JUN-1998; 98US-0089953P.

PR 19-JUN-1998; 98US-0089978P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.

PR 19-JUN-1998; 98US-0090078P.

PR 19-JUN-1998; 98US-0090079P.

PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.

XX

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX

PI Roberts BL, Shankara S;

XX

XX WPI; 2000-106077/09.

DR

XX

XX Isolated polynucleotides differentially expressed in antigen-presenting

PT cells, useful in gene vaccines against cancer.

PT

XX

PS Claim 1; Page 78; 130pp; English.

XX

CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene

CC expression) tags used to identify mRNA transcripts encoding

CC immunostimulatory cofactor proteins which are preferentially or

CC differentially expressed in monocyte-derived dendritic cells compared

CC with monocytes. Some of the transcripts correspond to known genes or ESTs

CC (expressed sequence tags) which were previously unknown to be

CC preferentially or differentially expressed in dendritic cells, while

CC other transcripts correspond to novel genes. Antigen-presenting cell

CC (APC)-associated costimulatory factors play an important role in the

CC activation of the cytotoxic immune response, particularly against tumour

CC cells. Tumour antigen presentation via the MHC (major histocompatibility

CC complex) and subsequent recognition by T-cell receptors is alone

CC insufficient to activate a robust cytotoxic immune response that can lyse

CC the tumour cells. Immunostimulatory cofactors also being required for

CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid

CC sequences identified using the SAGE tags have several potential uses.

CC They may be used in vaccines to induce an immune response, particularly

CC against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in

CC an APC; and as hybridisation probes/amplification primers for the

CC diagnosis, prognosis and monitoring of diseases related to abnormal

CC expression of these genes. Detection of the dendritic cell differentially

CC expressed genes, or of their encoded proteins, can be used to identify

CC cells as belonging to the monocyte lineage. Cells containing these genes

CC can be used in active immunotherapy (or to stimulate production of a

CC population of antigen-specific effector cells) and vectors containing

CC them are used in gene therapy. Co-administration of tumour antigens and

CC APC-associated costimulatory factors ensures adequate antigen

CC presentation to endogenous APCs and upregulates the APCs for the

CC presentation of co-stimulatory signals, migration to T cell-rich sites,

CC secretion of T cell growth factors and secretion of chemokines for

CC recruitment of immune effector cells

XX

XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

XX

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCGCTGGCA 15

Db 9 TAGCTGGCA 1

RESULT 291

AAZ78118

ID AAZ78118 standard; DNA; 10 BP.

XX

AC AAZ78118;

XX

XX 10-APR-2000 (first entry)

XX

DE Human dendritic cell SAGE tag, SEQ ID NO:546.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;

KW immunostimulatory cofactor; costimulatory factor; CTL;

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

OS WO9965924-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089911P.

PR 19-JUN-1998; 98US-0089922P.

PR 19-JUN-1998; 98US-0089933P.

PR 19-JUN-1998; 98US-0089944P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090038P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.

PR 19-JUN-1998; 98US-0090078P.

PR 19-JUN-1998; 98US-0090079P.

PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.

PA (ROBE) ROBERTS B L.

PA (SHAN) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

PT Claim 1; Page 80; 130pp; English.

PS Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells. Immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid

CC sequences identified using the SAGE tags have several potential uses.

CC They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX

SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCA 19

Db 2 TGGCAGGCA 10

RESULT 292

AAZ78051

ID AAZ78051 standard; DNA; 10 BP.

AC AAZ78051;

XX 10-APR-2000 (first entry)

DT Human dendritic cell SAGE tag, SEQ ID NO:479.

XX SAGE tag; serial analysis of gene expression; antigen presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;

KW immunostimulatory cofactor; costimulatory factor; CTL;

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

OS WO9965924-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089911P.

PR 19-JUN-1998; 98US-0089922P.

PR 19-JUN-1998; 98US-0089933P.

PR 19-JUN-1998; 98US-0089944P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090038P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

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PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
DR
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
PT
XX
XX Claim 1; Page 78; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells. Immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
XX Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e-02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 6 CTCGCTGGC 14
    |||
DB 2 CTCGCTGGC 10

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RESULT 293
AAZ78139/C
ID AAZ78139 standard; DNA; 10 BP.
XX
XX AAZ78139;
XX
XX 10-APR-2000 (first entry)
DT

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```

XX DE Human dendritic cell SAGE tag, SEQ ID NO:567.
XX
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
XX immunostimulatory cofactor; costimulatory factor; CTL;
XX cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX OS Homo sapiens.
XX
XX FN WC9965924-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013800.
XX
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089911P.
XX PR 19-JUN-1998; 98US-0089922P.
XX PR 19-JUN-1998; 98US-0089933P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089977P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
PT
XX
XX Claim 1; Page 81; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells. Immunostimulatory cofactors also being required for

```

efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen, to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14

Db 10 CTCGCTGGC 2

RESULT 294

AAZ78796

ID AAZ78796 standard; DNA; 10 BP.

XX AAZ78796;

XX 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:1224.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

OS Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089911P.

PR 19-JUN-1998; 98US-0089922P.

PR 19-JUN-1998; 98US-0089933P.

PR 19-JUN-1998; 98US-0089944P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.

PA (SOBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX MPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

XX Claim 1; Page 100; 130pp; English.

Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19

Db 2 TGGCAGCA 10

RESULT 295

AAZ77705

ID AAZ77705 standard; DNA; 10 BP.

XX AAZ77705;

XX AC

XX

DT 10-APR-2000 (first entry)
 XX Human dendritic cell SAGE tag, SEQ ID NO:133.
 DE
 DE
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013800.
 XX
 XX 19-JUN-1998; 98US-0089833P.
 XX 19-JUN-1998; 98US-0089844P.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089878P.
 XX 19-JUN-1998; 98US-0089991P.
 XX 19-JUN-1998; 98US-0089992P.
 XX 19-JUN-1998; 98US-0089993P.
 XX 19-JUN-1998; 98US-0089994P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0089999P.
 XX 19-JUN-1998; 98US-0090000P.
 XX 19-JUN-1998; 98US-0090035P.
 XX 19-JUN-1998; 98US-0090036P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.
 XX 19-JUN-1998; 98US-0090041P.
 XX 19-JUN-1998; 98US-0090042P.
 XX 19-JUN-1998; 98US-0090043P.
 XX 19-JUN-1998; 98US-0090044P.
 XX 19-JUN-1998; 98US-0090045P.
 XX 19-JUN-1998; 98US-0090047P.
 XX 19-JUN-1998; 98US-0090048P.
 XX 19-JUN-1998; 98US-0090072P.
 XX 19-JUN-1998; 98US-0090076P.
 XX 19-JUN-1998; 98US-0090077P.
 XX 19-JUN-1998; 98US-0090078P.
 XX 19-JUN-1998; 98US-0090079P.
 XX 19-JUN-1998; 98US-0090080P.
 XX 08-DEC-1998; 98US-0111715P.
 XX
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX
 XX WPI, 2000-106077/09.
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 67; 130pp; English.
 XX
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 XX expression) tags used to identify mRNA transcripts encoding
 XX immunostimulatory cofactor proteins which are preferentially or
 XX differentially expressed in monocyte-derived dendritic cells compared
 XX with monocytes. Some of the transcripts correspond to known genes or ESTs
 XX (expressed sequence tags) which were previously unknown to be
 XX preferentially or differentially expressed in dendritic cells, while
 XX other transcripts correspond to novel genes. Antigen-presenting cell
 XX (APC)-associated costimulatory factors play an important role in the
 XX activation of the cytotoxic immune response, particularly against tumour
 XX cells. Tumour antigen presentation via the MHC (major histocompatibility
 XX complex) and subsequent recognition by T-cell receptors is alone
 XX insufficient to activate a robust cytotoxic immune response that can lyse

CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CTCGCTGCG 14
 Db 2 CTCGCTGCG 10
 RESULT 296
 AAZ85223
 ID AAZ85223 standard; DNA; 10 BP.
 XX
 XX AAZ85223;
 XX
 XX 07-APR-2000 (first entry)
 XX
 XX Metastatic breast tumour cell downregulated transcript tag #4457.
 DE
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO9965928-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.
 XX 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX
 XX WPI, 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.
 XX
 XX Claim 1; Page 178; 219pp; English.
 XX

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
 |||||
 Db 2 CGCTGGTAC 10

RESULT 297
 AAZ81248/c
 ID AAZ81248 standard; DNA; 10 BP.

XX AC AAZ81248;
 XX
 DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #482.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.
 CS
 XX WO9965928-A2.
 XX
 PD 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

PS Claim 1; Page 71; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX

SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
 |||||
 Db 10 ACACGCTGG 2

RESULT 298
 AAZ82071/c
 ID AAZ82071 standard; DNA; 10 BP.

XX AC AAZ82071;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #1305.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.
 CS
 XX WO9965928-A2.
 XX
 PD 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.
XX Claim 1; Page 93; 219pp; English.
PS
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GGCACGAC 20
Db 9 GGCACGAC 1
|||||
|
RESULT 299
AAZ80823
ID AAZ80823 standard; DNA; 10 BP.
XX
AC AAZ80823;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #57.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX

PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 59; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GGCACGAC 20
Db 1 GGCACGAC 9
|||||
|
RESULT 300
AAZ83828
ID AAZ83828 standard; DNA; 10 BP.
XX
AC AAZ83828;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #3062.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX

DR WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 140; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CGCTGGCAC 16
Db 2 CACTGGCAC 10
RESULT 301
AAZ84731
ID AAZ84731 standard; DNA; 10 BP.
AC AAZ84731;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3965.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX

PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 164; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CTCGCTGGC 14
Db 2 CTTGCTGGC 10
RESULT 302
AAZ84972
ID AAZ84972 standard; DNA; 10 BP.
XX
AC AAZ84972;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4206.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA

(SHAN/) SHANKARA S.
 Roberts BL, Shankara S;
 WPI; 2000-106079/09.
 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
 Claim 1; Page 171; 219pp; English.
 AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGTCTG 12
 |||||
 Db 1 GACTCTCTG 9

RESULT 303
 AAZ85114
 ID AAZ85114 standard; DNA; 10 BP.
 AC AAZ85114;
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #4348.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.
 XX 19-JUN-1998; 98US-0090041P.

(GENZ) GENZYME CORP.
 (ROBE/) ROBERTS B L.
 (SHAN/) SHANKARA S.
 Roberts BL, Shankara S;
 WPI; 2000-106079/09.
 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
 Claim 1; Page 175; 219pp; English.
 AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
 |||||
 Db 2 GGACTCACT 10

RESULT 304
 AAZ86280
 ID AAZ86280 standard; DNA; 10 BP.
 AC AAZ86280;
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell downregulated transcript tag #5514.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.


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PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 170; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 85.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 TGGCAGCGCA 19
Db 2 TGGCAGACA 10
|||||
RESULT 307
AAZ85384/c
ID AAZ85384 standard; DNA; 10 BP.
AC AAZ85384;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4618.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX

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PF 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 183; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 GCTGGCAGC 17
Db 9 GCTGGCAGC 1
|||||
RESULT 308
AAZ86285/c
ID AAZ86285 standard; DNA; 10 BP.
XX
XX AAZ86285;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #5519.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX

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PD 23-DEC-1999.
XX PF
XX 18-JUN-1999; 99WO-US013647.
XX PF
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX PI
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS
XX Claim 1; Page 204; 219pp; English.
XX CC
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX SQ
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 10 GGCACACAC 2
|||||
|

RESULT 309
AAZ85204
ID AAZ85204 standard; DNA; 10 BP.
XX AC
XX AAZ85204;
XX AC
XX 07-APR-2000 (first entry)
XX DT
XX Metastatic breast tumour cell downregulated transcript tag #4438.
XX DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS
XX Homo sapiens.
XX KW

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FN WO9965928-A2.
XX PD
XX 23-DEC-1999.
XX PF
XX 18-JUN-1999; 99WO-US013647.
XX PF
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX PI
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS
XX Claim 1; Page 178; 219pp; English.
XX CC
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX SQ
XX Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGCACGC 18
Db 2 CAGGCACGC 10
|||||
|

RESULT 310
AAZ84046/c
ID AAZ84046 standard; DNA; 10 BP.
XX AC
XX AAZ84046;
XX AC
XX 07-APR-2000 (first entry)
XX DT
XX Metastatic breast tumour cell downregulated transcript tag #3280.
XX DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS
XX Homo sapiens.
XX KW

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OS Homo sapiens.
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 146; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 CTGGCAGGC 18
 |||||
 Db 10 CTGGCAGGC 2
 |||||
 RESULT 311
 AAZ81436
 ID AAZ81436 standard; DNA; 10 BP.
 XX
 AC AAZ81436;
 XX
 XX 07-APR-2000 (first entry)
 XX
 DT Metastatic breast tumour cell upregulated transcript tag #670.
 XX
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW

KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 76; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 CTGGCAGGC 18
 |||||
 Db 1 CTGGCAGGC 9
 |||||
 RESULT 312
 AAZ85659/c
 ID AAZ85659 standard; DNA; 10 BP.
 XX
 AC AAZ85659;
 XX
 XX 07-APR-2000 (first entry)
 XX
 DT Metastatic breast tumour cell downregulated transcript tag #4893.
 DE
 KW

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 PN 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 PF 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 PT Claim 1; Page 189; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCA 19
 |||||
 Db 10 TGGCACACA 2
 RESULT 313
 AAZ81131/C
 ID AAZ81131 standard; DNA; 10 BP.
 XX AAZ81131;
 AC AAZ81131;
 XX DT 07-APR-2000 (first entry)
 XX

DE Metastatic breast tumour cell upregulated transcript tag #365.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 PN 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 PF 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 PT Claim 1; Page 68; 219pp; English.
 PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGCTGGCAC 16
 |||||
 Db 10 CGCTGGCGC 2
 RESULT 314
 AAZ83254
 ID AAZ83254 standard; DNA; 10 BP.
 XX AAZ83254;
 AC AAZ83254;
 XX

DT 07-APR-2000 (first entry)
 XX Metastatic breast tumour cell upregulated transcript tag #2489.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090003P.
 PR 19-JUN-1998; 98US-0090004P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE) ROBERTS B.L.
 PA (SHAN) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 126; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GGCACGCAC 20
 DB 1 GGCACGCAC 9
 RESULT 315
 AAA56564/c
 ID AAA56564 standard; DNA; 10 BP.
 XX

AC AAA56564;
 XX 07-SEP-2000 (first entry)
 XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:458.
 DE Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterization;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.
 XX Homo sapiens.
 OS WO200024892-A1.
 PN 04-MAY-2000.
 XX 28-OCT-1999; 99WO-JP005982.
 XX 28-OCT-1998; 98JP-00307532.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Hashimoto S, Matsushima K, Suzuki T;
 PI WPI; 2000-350734/30.
 XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.
 XX Claim 49; Page 130; 138pp; Japanese.
 XX The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody
 CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
 CC specifically claimed oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages
 XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GGACTCGCT 11
 DB 10 GGACTCGCT 2
 RESULT 316
 AAA13669
 ID AAA13669 standard; DNA; 10 BP.
 XX AAA13669;
 AC AAA13669;
 XX 21-JUL-2000 (first entry)
 DT DNA-PEG conjugation DNA 10-mer oligonucleotide SEQ ID NO:1.
 DE Parallel select; diagnosis; pharmaceutical; agricultural; identification;
 XX

CC heterologous gene that is operably linked to a 5' regulatory region and a
 CC 3' termination sequence, in an expression vector is useful for expressing
 CC a heterologous gene which involves transforming a host cell with the
 CC expression vector. (I) confers properties such as localisation, transport
 CC and increased translation efficiency of a heterologous mRNA transcript
 CC when transcribed into such mRNA. (I) present in a vector is useful for
 CC increasing translation of a heterologous gene, by which increased
 CC production of recombinantly produced proteins in vivo on either a small,
 CC research scale or on a large commercial scale is increased. The
 CC recombinantly produced proteins whose translation is enhanced by (I) may
 CC be a biologically active protein, structural or therapeutic protein. (I)
 CC is useful in gene therapy. The present sequence represents an MBP
 CC consensus RNS decaucleotide sequence which is given in the
 CC exemplification of the present invention

XX SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTGCTGGC 14
 ||| |||||
 Db 9 CTCTCTGC 1

RESULT 319

AAI67389
 ID AAI67389 standard; DNA; 10 BP.

AC AAI67389;

XX 11-FEB-2002 (first entry)

DE Human FKBP8 gene polymorphism detecting primer.

XX FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
 KW immunosuppression; human; primer; ss.
 XX Homo sapiens.

XX WO200172965-A2.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-US009718.

XX 24-MAR-2000; 2000US-0192125P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Bentivegna SC, Choi JY, Klem SE, Koshy B;

XX Stephens JC;

XX WPI; 2001-626261/72.

XX New haplotypes of the FK506-binding protein 8 gene, useful for genotyping
 PT that gene in individual and to design new therapy for associated disease
 PT such as immunosuppression and cancer.
 XX Claim 16; Page 15; 98pp; English.

XX The invention relates to haplotyping the FK506-binding protein 8 (38kd)
 CC (FKBP8) gene in an individual. The method involves determining the
 CC identity of the nucleotide pair at one or more polymorphic sites selected
 CC from P1 to P26 (described in the specification). The invention is useful
 CC to improve the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC FKBP8 activity, for example immunosuppression and cancer. Sequences
 CC AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene
 CC polymorphisms by primer extension techniques

XX SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCACCC 18
 ||| |||||
 Db 1 CTGGCACCC 9

RESULT 320

AAI67391
 ID AAI67391 standard; DNA; 10 BP.

AC AAI67391;

XX 11-FEB-2002 (first entry)

DE Human FKBP8 gene polymorphism detecting primer.

XX FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
 KW immunosuppression; human; primer; ss.
 XX Homo sapiens.

XX WO200172965-A2.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-US009718.

XX 24-MAR-2000; 2000US-0192125P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Bentivegna SC, Choi JY, Klem SE, Koshy B;

XX Stephens JC;

XX WPI; 2001-626261/72.

XX New haplotypes of the FK506-binding protein 8 gene, useful for genotyping
 PT that gene in individual and to design new therapy for associated disease
 PT such as immunosuppression and cancer.
 XX Claim 16; Page 15; 98pp; English.

XX The invention relates to haplotyping the FK506-binding protein 8 (38kd)
 CC (FKBP8) gene in an individual. The method involves determining the
 CC identity of the nucleotide pair at one or more polymorphic sites selected
 CC from P1 to P26 (described in the specification). The invention is useful
 CC to improve the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC FKBP8 activity, for example immunosuppression and cancer. Sequences
 CC AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene
 CC polymorphisms by primer extension techniques

XX SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCACCC 18
 ||| |||||
 Db 2 CTGGCACCC 10

RESULT 321

AAI67386/C
 ID AAI67386 standard; DNA; 10 BP.

XX AAI67386;

XX

DT 11-FEB-2002 (first entry)
XX Human FKBP8 gene polymorphism detecting primer.
DE
XX
KW FKBP8-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
KW immunosuppression; human; primer; ss.
XX
OS Homo sapiens.
XX WO200172965-A2.
PN
XX
PD 04-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-US009718.
XX
XX 24-MAR-2000; 2000US-0192125P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Anastasio AE, Bentivegna SC, Choi JY, Kiem SE, Koshy B;
PI Stephens JC;
PI
XX
DR WPI; 2001-626261/72.
XX
XX New haplotypes of the FKBP8-binding protein 8 gene, useful for genotyping
PT that gene in individual and to design new therapy for associated disease
PT such as immunosuppression and cancer.
PT
XX
PS Claim 16; Page 15; 99pp; English.
XX
XX The invention relates to haplotyping the FKBP8-binding protein 8 (38kD)
CC (FKBP8) gene in an individual. The method involves determining the
CC identity of the nucleotide pair at one or more polymorphic sites selected
CC from P1 to P26 (described in the specification). The invention is useful
CC to improve the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC FKBP8 activity, for example immunosuppression and cancer. Sequences
CC AA16732-403 represent oligonucleotide primers for detecting FKBP8 gene
CC polymorphisms by primer extension techniques
XX
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GGCACGCCAC 20
DB 10 GGCACGCCAC 2
XX
RESULT 322
AAH63517
ID AAH63517 standard; cDNA; 10 BP.
XX
XX AAH63517;
AC
XX
XX 20-SEP-2001 (first entry)
DT Human ubiquitously expressed transcriptome sequence SEQ ID NO: 357.
DE
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
KW
XX Homo sapiens.
OS
XX WO200138577-A2.
FN
XX
XX 31-MAY-2001.
PD
XX 21-NOV-2000; 2000WO-US031922.
PF
XX 24-NOV-1999; 99US-00448480.
XX

XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
PT
XX
XX Claim 13; Page 47; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
XX
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 TCGCTGGCA 15
DB 1 TCGCTGGCA 9
XX
RESULT 323
AAH63853
ID AAH63853 standard; cDNA; 10 BP.
XX
XX AAH63853;
AC
XX 20-SEP-2001 (first entry)
DT Human ubiquitously expressed transcriptome sequence SEQ ID NO: 693.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
KW
XX Homo sapiens.
OS
XX WO200138577-A2.
PN
XX 31-MAY-2001.
PD
XX 21-NOV-2000; 2000WO-US031922.
PF
XX 24-NOV-1999; 99US-00448480.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX WPI; 2001-367706/38.
DR
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
PT
XX
XX Claim 13; Page 55; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC expressed in humans. They can also be used to screen for drugs, reduce

CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CTGCACGC 18

Db 2 CAGGCACGC 10

RESULT 324

AAH64386
ID AAH64386 standard; cDNA; 10 BP.

XX AC AAH64386;

DT 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1226.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,

XX such as cancer cell, comprises transcriptomes expressed in particular

XX cell types.

XX Claim 13; Page 67; 94pp; English.

XX The present invention describes a method of identifying the type of cell

XX in a sample, involving determining which of the sequences AAH63161-

XX AAH64724 is expressed by the cell. The transcriptomes described in the

XX invention are cell-type specific, cancer specific or ubiquitously

XX expressed in humans. They can also be used to screen for drugs, reduce

XX cancer specific gene expression, standardise expression and restore the

XX function of a diseased cell or tissue. The present sequence is one of the

XX transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19

Db 2 TGGCAGCA 10

RESULT 325

AAH64387

ID AAH64387 standard; cDNA; 10 BP.

XX AC AAH64387;

DT 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1227.

DE Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,

XX such as cancer cell, comprises transcriptomes expressed in particular

XX cell types.

XX Claim 13; Page 67; 94pp; English.

XX The present invention describes a method of identifying the type of cell

XX in a sample, involving determining which of the sequences AAH63161-

XX AAH64724 is expressed by the cell. The transcriptomes described in the

XX invention are cell-type specific, cancer specific or ubiquitously

XX expressed in humans. They can also be used to screen for drugs, reduce

XX cancer specific gene expression, standardise expression and restore the

XX function of a diseased cell or tissue. The present sequence is one of the

XX transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19

Db 2 TGGCAGCA 10

RESULT 326

AAH64528

ID AAH64528 standard; cDNA; 10 BP.

XX AC AAH64528;

DT 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1368.

DE Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX

```

PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu VE, Vogelstein B, Kinzler KW;
XX
PI WPI; 2001-367706/38.
XX
DR
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX
PS Claim 13; Page 70; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GGCACGCAC 20
DB 1 GGCACGCAC 9

RESULT 327
AAH63816
ID AAH63816 standard; cDNA; 10 BP.
XX
AC AAH63816;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 656.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu VE, Vogelstein B, Kinzler KW;
XX
PI WPI; 2001-367706/38.
XX
DR
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX
PS Claim 13; Page 54; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously

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CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX
SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 CTCGCTGGC 14
DB 2 CTCGCTGGC 10

RESULT 328
AAH64282
ID AAH64282 standard; cDNA; 10 BP.
XX
AC AAH64282;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1122.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu VE, Vogelstein B, Kinzler KW;
XX
PI WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX
PS Claim 11; Page 65; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 TGGCAGGCA 19
DB 2 TGGCAGGCA 10

RESULT 329
AAC86370/c

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ID AAC86370 standard; DNA; 10 BP.
 XX AC AAC86370;
 XX AC AAC86370;
 DT 01-MAR-2001 (first entry)
 XX DE Linker used to make pHR7.
 XX DE
 XX KW Lentivirus; HIV; human immunodeficiency virus; cystic fibrosis;
 KW KW Huntington's; Parkinson's; Alzheimer's disease; ss.
 OS Synthetic.
 XX OS
 XX PN WO20006759-A1.
 XX PD 09-NOV-2000.
 XX PF 26-APR-2000; 2000WO-US011097.
 XX PR 29-APR-1999; 99US-0131671P.
 XX PA (CELL-) CELL GENESYS INC.
 XX PI Naldini L, Dull T, Bukovsky A, Farson D, Witt R;
 XX PF 2001-007231/01.
 XX PF Disarmed lentiviral vector such as packaging and transfer vectors that
 PT direct the synthesis of lentiviral vector transcripts and lentiviral
 PT proteins, for rapid production of recombinant lentivirus.
 XX PS Example 7; Page 42; 80pp; English.
 XX CC The present invention relates to a lentivirus transfer vector with
 CC modified 5' long terminal repeat (LTR) and 3' LTR. The vector is useful
 CC for producing a recombinant lentivirus in mammalian cells. The virus is
 CC useful for in vivo and ex vivo transfer and expression of nucleic acid
 CC sequences. The recombinant lentivirus is useful for treating HIV-infected
 CC cells, cystic fibrosis, Huntington's disease, Parkinson's disease and
 CC Alzheimer's disease. The vector is also useful for synthesizing
 CC lentiviral vector transcripts which can be packaged and lentiviral
 CC proteins for rapid production of high titer recombinant lentivirus in
 CC mammalian cells
 XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGCACTCG 9
 DB 10 ATTGACTCG 2
 RESULT 330
 ID AAF70422 standard; DNA; 10 BP.
 XX AC AAF70422;
 XX AC AAF70422;
 DT 20-APR-2001 (first entry)
 XX DE Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:165.
 XX KW Human; dopamine receptor D2; DRD2; polymorphism; allele specific;
 KW KW drug target isogene; detection; single nucleotide polymorphism; SNP;
 KW KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; WD;
 KW KW probe; PCR primer; ss.
 XX OS
 XX OS Homo sapiens.
 XX PN WO200105832-A1.

XX PD 25-JAN-2001.
 XX PF 19-JUL-2000; 2000WO-US019644.
 XX PR 19-JUL-1999; 99US-014493P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 XX PF 2001-091967/10.
 XX PF Polynucleotides comprising single nucleotide polymorphisms in the human
 PT dopamine receptor D2, useful for detecting mutations associated with,
 PT e.g. schizophrenia, Parkinson's and myoclonus dystonia.
 XX PS Disclosure; Page 24; 135pp; English.
 XX CC The present invention describes polynucleotides comprising single
 CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).
 CC The polynucleotides may be used in assays to detect and characterise
 CC polymorphisms in DRD2 that affect its expression and activity and are
 CC involved in disorders such as schizophrenia, Parkinson's and myoclonus
 CC dystonia (MD). This information would be useful for studying the
 CC biological function of DRD2 as well as in identifying drugs targeting
 CC this protein for the treatment of disorders related to its abnormal
 CC expression or function. Polymorphisms in the DRD2 gene affect the
 CC expression of active and functional polypeptides. Therefore it is
 CC advantageous to detect polymorphisms in the DRD2 gene and how those
 CC polymorphisms are combined in different copies of the gene. AAF70261 to
 CC AAF70309 represent human DRD2 allele specific oligonucleotide probes, and
 CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
 CC primers which are used in the detection of DRD2 polymorphisms. AAF70405
 CC to AAF70452 represent oligonucleotide primers for the detection of human
 CC DRD2 polymorphisms which are given in the exemplification of the present
 CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
 CC gene which are used in examples from the present invention
 XX SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TCGCTGGCA 15
 DB 9 TCGCTGCA 1
 RESULT 331
 ID ABA83149 standard; cDNA; 10 BP.
 XX AC ABA83149;
 XX AC ABA83149;
 DT 08-FEB-2002 (first entry)
 XX DE Ceruloplasmin (ferroxidase) ovarian tumour marker SAGE tag, #109.
 XX KW Ovarian tumour marker gene; human; overexpression; upregulation;
 KW KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW KW identification; serous cystadenoma; borderline serous tumour;
 KW KW mucinous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW KW undifferentiated carcinoma; borderline mucinous tumour; endometrioid carcinoma;
 KW KW adenofibroma; Brenner tumour; clear cell adenocarcinoma; cystadenofibroma;
 KW KW immune response pathway; cell proliferation regulation; protein folding;
 KW KW membrane localised; secreted; therapeutic target; cytostatic;
 KW KW gene therapy; vaccine; SAGE tag; ss.
 XX OS
 XX OS Homo sapiens.

PN WO200175177-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010947.
 XX
 PR 03-APR-2000; 2000US-0194336P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 XX
 DR WPI; 2001-626450/72.
 XX
 PT Detecting and identifying ovarian tumor, identifying increased risk for
 XX developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.
 XX
 PS Claim 26; Page 41; 140pp; English.
 XX
 CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumors in an individual via the detection and measurement of the
 CC expression of ovarian tumor marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumor in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumor as
 CC being an ovarian tumor (i.e., an epithelial ovarian tumor selected from
 CC serous cystadenoma, borderline serous tumor, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumor, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumor). The ovarian tumor marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumor cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumor marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183 represent SAGE tags derived from the ovarian tumor
 CC marker genes of the invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCA 19
 |||||
 Db 10 TGGCAGCA 2
 RESULT 332
 AAF41238/c
 ID AAF41238 standard; DNA; 10 BP.
 XX
 AC AAF41238;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7977.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 284; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC anticfungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle; the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 GCTGGCAGC 17
 |||||
 Db 9 GCAGGCAGC 1
 RESULT 333
 AAF42074
 ID AAF42074 standard; DNA; 10 BP.
 XX
 AC AAF42074;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8813.

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XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 314; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF3268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GACTGCTG 12
Db 1 GAGTCGCTG 9
RESULT 334
AAAF35970
ID AAF35970 standard; DNA; 10 BP.
XX
AC AAF35970;
XX

DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2709.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 96; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF3268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGACTCGCT 11
Db 1 GGACTCGCTT 9
RESULT 335
AAAF37397/C
ID AAF37397 standard; DNA; 10 BP.

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XX AAF37397;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4136.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 147; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACTCGCTGG 13
DB 9 ACGCGTGG 1

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RESULT 336
AAF40204
ID AAF40204 standard; DNA; 10 BP.
XX
XX AAF40204;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6943.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 248; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACTCTG 9
DB 1 ATGACTCTG 1

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Db 1 ATGGAGTCG 9

RESULT 337
AAAF41236/c
ID AAFA1236 standard; DNA; 10 BP.
XX AC
XX AC
XX AAFA1236;
XX DT
XX 23-MAR-2001 (first entry)
XX DE
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7975.
XX DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS
XX Saccharomyces cerevisiae.
XX FN
XX WO200077214-A2.
XX XX
XX 21-DEC-2000.
XX PF
XX 14-JUN-2000; 2000WO-US016223.
XX ER
XX 16-JUN-1999; 99US-00335032.
XX PA
XX (UYJO) UNIV JOHNS HOPKINS.
XX PI
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX DR
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS
XX Example; Page 284; 419pp; English.
XX CC
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAFA1236 to AAFA4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAFA12362 to AAFA33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ
XX Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GCTGGCAGC 17
Db 9 GCTGGCAGC 1

RESULT 338
AAFA43023
ID AAFA43023 standard; DNA; 10 BP.
XX AC
XX AAFA43023;
XX DT
XX 23-MAR-2001 (first entry)
XX DE
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:111362.
XX KW
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS
XX Saccharomyces cerevisiae.
XX FN
XX WO200077214-A2.
XX XX
XX 21-DEC-2000.
XX PF
XX 14-JUN-2000; 2000WO-US016223.
XX ER
XX 16-JUN-1999; 99US-00335032.
XX PA
XX (UYJO) UNIV JOHNS HOPKINS.
XX PI
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX DR
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS
XX Example; Page 348; 419pp; English.
XX CC
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAFA43023 to AAFA4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAFA430232 to AAFA33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 CTCGCTGGC 14
 11 |||||
 Db 2 CTGGCTGGC 10
 11 |||||

RESULT 339
 AAF40185/c
 ID AAF40185 standard; DNA; 10 BP.
 XX
 AC AAF40185;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6924.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-USO16223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 247; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 TGGCAGGCA 19
 11 |||||
 Db 10 TGGCAGGCA 2
 10 |||||

RESULT 340
 AAF43779
 ID AAF43779 standard; DNA; 10 BP.
 XX
 AC AAF43779;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11918.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-USO16223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 375; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 TGGACTCGC 10
 |||||
 Db 2 TGGCTCGC 10
 |||||
 RESULT 341
 AAF35822
 ID AAF35822 standard; DNA; 10 BP.
 AC AAF35822;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2561.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 91; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame, or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 7 TCGCTGGCA 15
 |||||
 Db 2 TCGCTGGTA 10
 |||||
 RESULT 342
 AAF41117/c
 ID AAF41117 standard; DNA; 10 BP.
 XX
 AC AAF41117;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7856.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 280; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame, or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially

CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
Db 9 AAGGACTCG 1
RESULT 343
AAF39261/c
ID AAF39261 standard; DNA; 10 BP.
XX AAF39261;
AC AAF39261;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6000.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; da.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 214; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
Db 9 GGACTCGCT 1
RESULT 344
AAF36425/c
ID AAF36425 standard; DNA; 10 BP.
XX AAF36425;
AC AAF36425;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3154.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; da.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 113; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGACTCG 9
 Db 9 ATTGACTCG 1
 RESULT 345
 AAF43192/c
 ID AAF43192 standard; DNA; 10 BP.
 XX
 AC AAF43192;
 DT 23-MAR-2001 (first entry)
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11331.
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 FN
 XX 21-DEC-2000.
 PD
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 354; 419pp; English.
 PS
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCGCA 19
 Db 9 TTGACGCA 1
 RESULT 346
 AAF43700
 ID AAF43700 standard; DNA; 10 BP.
 XX
 AC AAF43700;
 DT 23-MAR-2001 (first entry)
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11839.
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 FN
 XX 21-DEC-2000.
 PD
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 372; 419pp; English.
 PS
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGACTCGC 10
 Db 1 TTGACTCGC 9

RESULT 347
 AAF41118/c
 ID AAF41118 standard; DNA; 10 BP.
 XX AAF41118;
 AC AAF41118;
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7857.
 DE Yeast;
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS
 XX WO200077214-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 280; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACTCGC 9
 Db 9 ATGACTCGC 1

RESULT 348
 AAF43100
 ID AAF43100 standard; DNA; 10 BP.
 XX AAF43100;
 AC AAF43100;
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11239.
 DE Yeast;
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS
 XX WO200077214-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 351; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag, also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCGTGTG 12
 |||||
 Db 2 GACTCGTGTG 10

RESULT 349
 AAF43372/C
 ID AAF43372 standard; DNA; 10 BP.

AC AAF43372;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11511.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

FN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 361; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag, also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGCTGGCAC 16

|||
 Db 10 CGATGGCAC 2

RESULT 350

AAF40677/C

ID AAF40677 standard; DNA; 10 BP.

XX AAF40677;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7416.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 264; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

QY 4 GACTGCTGT 12
 |||||
 DB 9 GACTGCTGT 1

RESULT 351
 AAF38331/C
 ID AAF38331 standard; DNA; 10 BP.

XX AAF38331;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5070.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO20007214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 181; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

QY 11 TGGCAGCGCA 19
 |||||
 DB 10 TGTCAAGCA 2

RESULT 352

AA518719

ID AA518719 standard; DNA; 10 BP.

XX AA518719;

XX 12-MAR-2002 (first entry)

XX Primer-extension oligonucleotide #7 to detect human SCYA3 polymorphisms.
 DE nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 KW small inducible cytokine A3; haplotyping; genotyping; primer; ss;
 KW inflammatory disorder.

XX Homo sapiens.

XX WO200179217-A2.

XX 25-OCT-2001.

XX 30-MAR-2001; 2001WO-US010595.

XX 14-APR-2000; 2000US-0197830P.

XX (GENA-) GENAISANCE PHARM INC.

XX Chew A, Choi JY, Koshi B, Stephens JC;
XX WPI; 2002-055247/07.
XX New polymorphic variants comprising small inducible cytokine A3 (SCYA3)
XX isogene, useful in expressing SCYA3 protein for use in screening for
XX candidate drugs to treat diseases related to SCYA3 activity, e.g.
XX inflammatory disorders.
XX Claim 17; Page 15; 67pp; English.
XX The present invention relates to novel single nucleotide polymorphisms
XX (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on
XX chromosome 17q11-q21, and methods for haplotyping and/or genotyping the
XX SCYA3 gene. The methods of the invention make use of allele-specific
XX oligonucleotides (ASOs) as probes and primers and/or primer-extension
XX oligonucleotides for detecting the SCYA3 gene polymorphisms. The
XX polymorphisms and screened compounds are useful for (developing)
XX treatment of diseases associated with SCYA3 activity, such as
XX inflammatory disorders e.g. atopic dermatitis, rheumatoid arthritis,
XX multiple sclerosis, pulmonary fibrosis and sarcoidosis. AAS18713-AAS18742
XX represent primer-extension oligonucleotides for detecting human SYCA3
XX gene polymorphisms
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACTCGCTGG 13
Db 2 ACTCTCTGG 10
|||||
RESULT 353
AAS18723 standard; DNA; 10 BP.
ID AAS18723
AC AAS18723;
XX AAS18723;
XX 12-MAR-2002 (first entry)
XX Primer-extension oligonucleotide #11 to detect human SCYA3 polymorphisms.
XX Human; single nucleotide polymorphism; SNP; SCYA3; chromosome 17q11-q21;
XX small inducible cytokine A3; haplotyping; genotyping; primer; ss;
XX inflammatory disorder.
XX Homo sapiens.
XX WO200179217-A2.
XX 25-OCT-2001.
XX 30-MAR-2001; 2001WO-US010595.
XX 14-APR-2000; 2000US-0197830P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Chew A, Choi JY, Koshi B, Stephens JC;
XX WPI; 2002-055247/07.
XX New polymorphic variants comprising small inducible cytokine A3 (SCYA3)
XX isogene, useful in expressing SCYA3 protein for use in screening for
XX candidate drugs to treat diseases related to SCYA3 activity, e.g.
XX inflammatory disorders.
XX Claim 17; Page 15; 67pp; English.

CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on
CC chromosome 17q11-q21, and methods for haplotyping and/or genotyping the
CC SCYA3 gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA3 gene polymorphisms. The
CC polymorphisms and screened compounds are useful for (developing)
CC treatment of diseases associated with SCYA3 activity, such as
CC inflammatory disorders e.g. atopic dermatitis, rheumatoid arthritis,
CC multiple sclerosis, pulmonary fibrosis and sarcoidosis. AAS18713-AAS18742
CC represent primer-extension oligonucleotides for detecting human SYCA3
CC gene polymorphisms
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 CTGACACGC 18
Db 1 CTGACACGC 9
|||||
RESULT 354
AAL45325 standard; DNA; 10 BP.
ID AAL45325
AC AAL45325;
XX 29-MAY-2002 (first entry)
XX Human KCNB1 gene primer extension oligo SEQ ID NO: 39.
XX Human; KCNB1; single nucleotide polymorphism; SNP; gene therapy;
XX potassium voltage-gated channel; Shab-related subfamily, member 1;
XX isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR;
XX primer extension oligonucleotide; ss.
XX Homo sapiens.
XX WO200204675-A1.
XX 17-JAN-2002.
XX 05-JUL-2001; 2001WO-US021307.
XX 05-JUL-2000; 2000US-0215885P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Chew A, Choi JY, Koshi B;
XX WPI; 2002-188469/24.
XX Isolated polymorphic variants of potassium voltage-gated channel, Shab-
XX related subfamily, member 1 (KCNB1) gene useful for expressing KCNB1
XX protein isoform to screen drugs to treat KCNB1 activity-related disease.
XX Claim 18; Page 14; 180pp; English.
XX The present invention provides the protein, gene and cDNA sequences of
XX the human potassium voltage-gated channel, Shab-related subfamily, member
XX 1 (KCNB1) isogene and polymorphisms identified within these sequences.
XX The sequences can be used to screen drugs, which involves contacting the
XX polypeptide with a candidate agent, and to assay for binding activity as
XX a target for drugs to treat arrhythmia and seizures. The present sequence
XX is a primer extension oligonucleotide described in the invention
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGCTGGCAC 16
| | | | |
Db 1 CGCTGTAC 9

RESULT 355
AAS18285
ID AAS18285 standard; DNA; 10 BP.
AC AAS18285;
XX
DT 25-FEB-2002 (first entry)
XX
DE Primer-extension oligonucleotide #5 to detect IMPDH2 gene polymorphisms.
XX
KW Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2;
KW IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic; primer;
KW ss.
XX
XX Homo sapiens.
XX
XX WO200177363-A2.
PN
XX
XX 18-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US011851.
PF
XX
XX 11-APR-2000; 2000US-0196248P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Chew A, Choi JY, Koehy B, Lee HH, Stephens JC;
PI
XX
XX WPI; 2002-041297/05.
DR
XX
XX New isolated polynucleotide having polymorphic variant of IMP2
PT dehydrogenase gene, useful for studying expression of the gene in vivo,
PT and for testing efficacy of therapeutic agents for cancer in biological
PT system.
XX
XX Claim 17; Page 13; 70pp; English.
PS
XX
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on
CC chromosome 3p21.2, and methods for haplotyping and/or genotyping the
CC IMPDH2 gene in an individual. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the IMPDH2 gene
CC polymorphisms. The polynucleotides and screened compounds are useful for
CC (developing) treatment of diseases associated with IMPDH2 activity, such
CC as cancer. AAS18280-AAS18305 represent primer-extension oligonucleotides
CC for detecting IMPDH2 gene polymorphisms
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCGCTG 12
| | | | |
Db 1 GCCTCGCTG 9

RESULT 356
AAS99299/C
ID AAS99299 standard; DNA; 10 BP.
XX
AC AAS99299;
XX
DT 12-MAR-2002 (first entry)

XX
DE Human F12 gene allele-specific oligonucleotide PCR primer #26.
XX
KW Human; coagulation factor XII; F12; haplotyping; haplotype pair; ss;
KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
KW coronary artery disease; liver disease; spontaneous abortion; cardiac;
KW Alzheimer's disease; blood coagulation; hepatotropic; neuroprotective;
KW neotropic; coagulant; antiabortive; sequencing primer; PCR primer; probe;
KW primer tail.
XX
XX Homo sapiens.
OS
XX
XX WO200179228-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 13-APR-2001; 2001WO-US012257.
PF
XX
XX 14-APR-2000; 2000US-0197837P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Bentivegna SC, Chew A, Choi JY, Nandabalan K;
PI
XX
XX WPI; 2002-075061/10.
DR
XX
XX Novel isolated human coagulation factor XII polynucleotide, F12 useful
PT for treatment of e.g. coronary artery disease, comprises a sequence which
PT is a polymorphic variant of a reference sequence for F12 gene or its
PT fragment.
XX
XX Claim 18; Page 14; 72pp; English.
PS
XX
XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human coagulation factor XII (F12) polypeptide. A method for
CC haplotyping the F12 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the F12 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the F12 gene can be identified
CC by comparing the frequency of the haplotype or haplotype pair in a
CC population exhibiting the trait with the frequency of the haplotype or
CC haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. F12 and its corresponding DNA are used
CC for studying the expression and function of F12, for use in screening for
CC candidate drugs to treat disorders related to F12 activity such as
CC coronary artery disease, liver disease, spontaneous abortion, Alzheimer's
CC disease and other diseases associated with defects in blood coagulation.
CC The sequences are also useful for studying the effect of variation on the
CC biological activity of F12 as well as on the binding affinity of
CC candidate drugs targeting F12. Sequences AAS99229-AAS99305 represent
CC probes, primers and primer tails used to detect F12 gene polymorphisms
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCTGGCAGC 17
| | | | |
Db 10 GCTTGACG 2

RESULT 357
ABK93938/C
ID ABK93938 standard; cDNA; 10 BP.
XX
XX ABK93938;
AC
XX

XX	ABK93921;	
XX	26-AUG-2002 (first entry)	
XX	Human protein kinase BAA34445.1 expressed sequence tag (EST) #10.	
XX	Human; protein kinase, cell-cell adhesion; neoplasm; melanoma; lung;	
KW	colorectal; breast; pancreas; head and neck tumour; solid tumour;	
KW	myeloproliferative disorder; leukaemia; non-Hodgkin lymphoma; shock;	
KW	leukopenia; thrombocytopenia; angiogenesis disorder; Kaposi's sarcoma;	
KW	inflammatory disease; allergy; inflammatory bowel disease; sepsis;	
KW	autoimmune disease; arthritis; psoriasis; asthma; thrombosis; pain;	
KW	respiratory tract inflammation; organ transplantation; angina; AIDS;	
KW	cardiovascular disease; hypertension; oedema; atherosclerosis;	
KW	reflexion injury; ischaemia; central nervous system disease; infection;	
KW	Alzheimer's disease; brain injury; amyotrophic lateral sclerosis;	
KW	renal disease; diabetes mellitus; osteoporosis; gene; EST; ss;	
KW	acquired immune deficiency syndrome; expressed sequence tag; BAA3445.1.	
OS	Homo sapiens.	
XX	WO200234901-A2.	
PN	02-MAY-2002.	
PD	24-OCT-2001; 2001WO-GB004719.	
PF	24-OCT-2000; 2000GB-00026004.	
XX	(INPH-) INPHARMATICA LTD.	
XX	Pagan RJ, Phelps CB, Nicholls RQ;	
PI	WPI; 2002-489944/52.	
DR	Novel protein kinase polypeptide useful for treating solid tumors,	
XX	inflammatory disease, autoimmune disease, arthritis, organ	
PT	transplantation, cardiovascular disease, central nervous system disease,	
PT	and infection.	
PS	Example 1; Fig 11; 94pp; English.	
XX	The invention relates to a protein kinase polypeptide (I), BAA34445.1,	
CC	and the encoding polynucleotide (II). (I) is useful as a protein kinase	
CC	and for effecting cell-cell adhesion. (II) is useful for expressing a	
CC	protein with kinase activity. (I) and (II) are useful in therapy or	
CC	diagnosis of disease and for treatment of neoplasm e.g. melanoma, lung,	
CC	colorectal, breast, pancreas, head and neck and other solid tumours,	
CC	myeloproliferative disorder, such as leukaemia, non-Hodgkin lymphoma,	
CC	leukopenia, thrombocytopenia, angiogenesis disorder, Kaposi's sarcoma,	
CC	inflammatory disease, such as allergy, inflammatory bowel disease,	
CC	autoimmune disease, arthritis, psoriasis and respiratory tract	
CC	inflammation, asthma, organ transplantation, cardiovascular disease,	
CC	hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock,	
CC	reflexion injury, ischaemia, central nervous system disease, including	
CC	Alzheimer's disease, brain injury and amyotrophic lateral sclerosis,	
CC	pain, renal disease, diabetes mellitus, osteoporosis, AIDS, viral	
CC	infection, bacterial infection, fungal infection and parasitic infection.	
CC	ABK93911-ABK93949 represent protein kinase coding sequences and related	
CC	expressed sequence tags of the invention	
XX	Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;	
SQ	Query Match 37.0%; Score 7.4; DB 1; Length 10;	
	Best Local Similarity 88.9%; Pred. No. 1.6e+02;	
	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	11 TGGCAGCGCA 19	
DB	10 TGGCAGCGCA 2	

RESULT 359
 ID ABK93949/c
 XX ABK93949 standard; cDNA; 10 BP.
 AC ABK93949;
 XX 26-AUG-2002 (first entry)
 DT
 XX Human protein kinase BAA34445.1 expressed sequence tag (EST) #38.
 DE
 XX Human; protein kinase; cell-cell adhesion; neoplasm; melanoma; lung;
 KW colorectal; breast; pancreas; head and neck tumour; solid tumour;
 KW myeloproliferative disorder; leukaemia; non-Hodgkin lymphoma; shock;
 KW leukopenia; thrombocytopenia; angiogenesis disorder; Kaposi's sarcoma;
 KW inflammatory disease; allergy; inflammatory bowel disease; sepsis;
 KW autoimmune disease; arthritis; psoriasis; asthma; thrombosis; pain;
 KW respiratory tract inflammation; organ transplantation; angina; AIDS;
 KW cardiovascular disease; hypertension; oedema; atherosclerosis;
 KW reperfusion injury; ischaemia; central nervous system disease; infection;
 KW Alzheimer's disease; brain injury; amyotrophic lateral sclerosis;
 KW renal disease; diabetes mellitus; osteoporosis; gene; EST; ss;
 KW acquired immune deficiency syndrome; expressed sequence tag; BAA3445.1.
 XX
 OS Homo sapiens.
 XX
 XX WO200234901-A2.
 PN
 XX 02-MAY-2002.
 PD
 XX 24-OCT-2001; 2001WO-GB004719.
 PF
 XX 24-OCT-2000; 2000GB-00026004.
 PR
 XX (INPH-) INPHARMATICA LTD.
 XX Pagan RJ, Phelps CB, Nicholls RQ;
 PI
 XX WPI; 2002-489944/52.
 DR
 XX Novel protein kinase polypeptide useful for treating solid tumors,
 PT inflammatory disease, autoimmune disease, arthritis, organ
 PT transplantation, cardiovascular disease, central nervous system disease,
 PT and infection.
 XX Example 1; Fig 11; 94pp; English.
 PS
 CC The invention relates to a protein kinase polypeptide (I), BAA34445.1,
 CC and the encoding polynucleotide (II). (I) is useful as a protein kinase
 CC and for effecting cell-cell adhesion. (II) is useful for expressing a
 CC protein with kinase activity. (I) and (II) are useful in therapy or
 CC diagnosis of disease and for treatment of neoplasm e.g. melanoma, lung,
 CC colorectal, breast, pancreas, head and neck and other solid tumours,
 CC myeloproliferative disorder, such as leukaemia, non-Hodgkin lymphoma,
 CC leukopenia, thrombocytopenia, angiogenesis disorder, Kaposi's sarcoma,
 CC inflammatory disease, such as allergy, inflammatory bowel disease,
 CC autoimmune disease, arthritis, psoriasis and respiratory tract
 CC inflammation, asthma, organ transplantation, cardiovascular disease,
 CC hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock,
 CC reperfusion injury, ischaemia, central nervous system disease, including
 CC Alzheimer's disease, brain injury and amyotrophic lateral sclerosis,
 CC pain, renal disease, diabetes mellitus, osteoporosis, AIDS, viral
 CC infection, bacterial infection, fungal infection and parasitic infection.
 CC ABK93949 represents protein kinase coding sequences and related
 CC expressed sequence tags of the invention
 XX
 XX Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 TGGCAGCA 19
 ||||| |||

Db 10 TGGCAGGCA 2
 RESULT 360
 ABK17006
 ID ABK17006 standard; DNA; 10 BP.
 XX ABK17006;
 AC ABK17006;
 XX 26-MAR-2002 (first entry)
 DT
 XX Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #29.
 DE
 XX Pyridoxal kinase; pyridoxine; vitamin B6;
 KW PDXK autoimmune polyglandular disease type 1; transgenic animal;
 KW gene therapy; primer extension; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200190125-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 24-MAY-2001; 2001WO-US016909.
 PF
 XX 24-MAY-2000; 2000US-0206664P.
 PR
 XX (GENA-) GENAISANCE PHARM INC.
 XX Chew A, Duda A, Koshy B;
 PI
 XX WPI; 2002-106169/14.
 DR
 XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polyNt, and for expressing pyridoxal protein.
 PT
 XX Claim 19; Page 14; 135pp; English.
 PS
 CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin
 CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
 CC studying the expression and function of PDXK, and in expressing PDXK
 CC protein for use in screening for candidate drugs to treat PDXK related
 CC diseases and for therapeutic purposes. A transgenic animal is useful for
 CC studying expression of the PDXK isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against PDXK protein, and for testing the
 CC efficacy of therapeutic agents and compounds for autoimmune polyglandular
 CC disease type 1. The polypeptide is useful for studying the effect of the
 CC variation on the biological activity of PDXK and the binding affinity of
 CC candidate drugs targeting PDXK for the treatment of autoimmune
 CC polyglandular disease type 1. Genotyping and haplotyping is useful for
 CC improving the efficacy and reliability of several steps in the discovery
 CC and development of drugs for treating diseases associated with PDXK
 CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK
 CC as a candidate agent for treating a specific condition or disease
 CC predicted to be associated with PDXK activity, and in the design of
 CC clinical trials of candidate drugs. This sequence is one of 38 (see
 CC ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by
 CC primer extension techniques, described in the method of the invention
 XX
 XX Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGCTGGCAC 16
 ||||| |||
 Db 2 CGCTGGCTC 10
 RESULT 361
 AAL48062/c

ID AAL48062 standard; DNA; 10 BP.
 XX
 AC AAL48062;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 40.
 XX
 KW Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;
 KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;
 KW neutropenia; promyelocytic leukaemia; haematological disorder;
 KW gene therapy; PCR; primer extension oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 DN WO200194364-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 11-JUN-2001; 2001WO-US018813.
 XX
 PR 09-JUN-2000; 2000US-0210380P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda A, Kazemi A, Messer C, Sausker EA;
 XX
 DR WPI; 2002-566435/60.
 XX
 XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
 PT improving efficiency and reliability in the development of drugs for
 PT treating diseases associated with CSF3 activity e.g. neutropenia.
 XX
 PS Claim 19; Page 13; 68pp; English.
 XX
 CC The present invention provides the protein, gene and cDNA sequences of
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.
 CC The sequences can be used in the treatment of neutropenia, promyelocytic
 CC leukaemia and haematological disorders. The present sequence is an allele
 CC specific primer extension oligonucleotide used to isolate the coding
 CC sequences of the invention
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 ACTCGCTGG 13
 Db |||||
 10 ACTCTCTGG 2
 RESULT 362
 ABQ71448/c
 ID ABQ71448 standard; DNA; 10 BP.
 XX
 AC ABQ71448;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:567.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX

PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX
 PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX
 PI Liu Q;
 XX
 DR WPI; 2002-500284/53.
 XX
 PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX
 PS Example 1; Page 43; 81pp; English.
 XX
 CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such that
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplex target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (II), (III) or (M) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABQ48191 to ABP51210 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGCTGGCAC 16
 Db |||||
 9 CGCTGGCAC 1
 RESULT 363
 ABQ71449/c
 ID ABQ71449 standard; DNA; 10 BP.
 XX
 AC ABQ71449;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:568.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX

PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 43; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (II) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
XX Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
SQ

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CGCTGGCAC 16
DB 9 CGCTGGCAC 1
|||||
|

RESULT 364
ABU57847/C
ID ABL57847 standard; RNA; 10 BP.
XX
XX ABL57847;
XX
XX 04-JUL-2002 (first entry)
XX
XX Hepatitis C virus internal ribosome entry site, IRES, IIIC loop.
XX
XX IRES; internal ribosome entry site; viral protein synthesis inhibition;
XX viral replication inhibition; viral infection; virucide; IIIC loop; ss.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FT stem_loop 1..10
FT /*tag= a
XX
XX FR2815358-A1.
XX
XX 19-APR-2002.
XX
XX 17-OCT-2000; 2000FR-00013303.
XX
XX 17-OCT-2000; 2000FR-00013303.
XX

PA (PART-) PARTEUROP DEV SA.
XX
XX Balakireva L;
XX
XX WPI; 2002-354321/39.
XX
XX Screening for polypeptide having mutant RNA recognition site, useful for
PT controlling viral infections, especially hepatitis C, by binding to
PT internal ribosome entry site.
XX
XX Claim 8; Page 34; 40pp; French.
XX
XX The present invention relates to a method for screening for a recombinant
CC polypeptide, which contains at least one mutant RNA recognition motif
CC (mMRR) for binding to an internal ribosome entry site (IRES), or one of
CC its domains. The recombinant polypeptide inhibits viral proteins
CC synthesis (and thus viral replication) in vivo and in vitro, by binding
CC to IRES in competition with cellular or viral proteins that normally bind
CC to it. Recombinant polypeptides identified by the invention are useful
CC for treatment or prevention of viral infection in which the replication
CC cycle includes a CAP-independent translation of an RNA sequence,
CC specifically hepatitis C virus, but also bovine/calf/human diarrhoea
CC viruses, swine pest, piglet transmissible gastro-enteritis, foot-and-
CC mouth disease, hepatitis A, murine hepatitis, common cold virus or avian
CC bronchitis. The present sequence is the IIC loop of the IRES from
CC Hepatitis C virus, which was used to illustrate the invention
XX
XX Sequence 10 BP; 0 A; 4 C; 5 G; 0 T; 1 U; 0 Other;
SQ

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GGCACGCCAC 20
DB 9 GGCACGCCAC 1
|||||
|

RESULT 365
ABV78428/C
ID ABV78428 standard; CDNA; 10 BP.
XX
XX AC ABV78428;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:139.
XX
XX SAGE tag; serial analysis of gene expression; human; Th1 cell;
XX activated T cell; T lymphocyte; immune response; expression pattern;
XX preferential expression; immune disorder; EST; expressed sequence tag;
XX ss.
XX
XX Homo sapiens.
XX
XX JP2002186482-A.
XX
XX 02-JUL-2002.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-594261/64.
XX
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
XX
XX Claim 19; Page 10; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC

CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
 CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells

XX SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
 Db 10 CGCTGGGCG 2
 |||||

RESULT 366
 ABV78506
 ID ABV78506 standard; cDNA; 10 BP.
 XX AC ABV78506;
 XX DT 29-NOV-2002 (first entry)
 XX DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:217.
 XX KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
 XX KW activated T cell; T lymphocyte; immune response; expression pattern;
 XX KW preferential expression; immune disorder; EST; expressed sequence tag;
 XX KW ss.
 XX OS Homo sapiens.
 XX PN JP2002186482-A.
 XX PD 02-JUL-2002.
 XX PF 19-DEC-2000; 2000JP-00385816.
 XX PR 19-DEC-2000; 2000JP-00385816.
 XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-594261/64.
 XX DR Human activated Th1 and Th2 cell expression gene group, useful for the
 XX PT diagnosis and treatment of Th1 and Th2-related diseases.
 XX PS Claim 19; Page 12; 60pp; Japanese.
 XX CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags

CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells

XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
 Db 1 GGAAATCGCT 9
 |||||

RESULT 367
 ABV84790
 ID ABV84790 standard; cDNA; 10 BP.
 XX AC ABV84790;
 XX DT 12-DEC-2002 (first entry)
 XX DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #600.
 XX KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 XX KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 XX KW expression pattern; differential expression; ss.
 XX OS Homo sapiens.
 XX PN JP2002209591-A.
 XX PD 30-JUL-2002.
 XX PF 19-JAN-2001; 2001JP-00012328.
 XX PR 19-JAN-2001; 2001JP-00012328.
 XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-631294/58.
 XX DR Human chronic hepatitis C tissue expression exasperating gene group
 XX PT comprises 100 high-ranking genes.
 XX PS Claim 46; Page 27; 139pp; Japanese.
 XX CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue

XX SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGC 10
 DB 1 TGGACGCGC 9

 RESULT 369
 ABV84695
 ID ABV84695 standard; cDNA; 10 BP.
 AC ABV84695;
 XX
 DT 12-DEC-2002 (first entry)
 DE
 DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #505.
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002209591-A.
 PD 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 PS Claim 46; Page 25; 139pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 GGACTCGCT 11
 DB 2 GGACGCGCT 10

 RESULT 369
 ABV84296
 ID ABV84296 standard; cDNA; 10 BP.
 AC ABV84296;
 XX
 DT 12-DEC-2002 (first entry)
 DE
 DE Human multiple chronic hepatitis C underexpressed genes SAGE tag #106.
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002209591-A.
 PD 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 PS Claim 10; Page 13; 139pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in chronic
 CC hepatitis C liver tissue compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 11 TGGCAGCCA 19
 DB 2 TGGCAGCCA 10

 RESULT 370
 ABV84523
 ID ABV84523 standard; cDNA; 10 BP.
 AC ABV84523;
 XX
 DT 12-DEC-2002 (first entry)
 DE
 DE Human HCC underexpressed gene SAGE tag #333.
 XX

ID ABV84296 standard; cDNA; 10 BP.
 AC ABV84296;
 XX
 DT 12-DEC-2002 (first entry)
 DE
 DE Human multiple chronic hepatitis C underexpressed genes SAGE tag #106.
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002209591-A.
 PD 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 PS Claim 10; Page 13; 139pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in chronic
 CC hepatitis C liver tissue compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 11 TGGCAGCCA 19
 DB 2 TGGCAGCCA 10

 RESULT 370
 ABV84523
 ID ABV84523 standard; cDNA; 10 BP.
 AC ABV84523;
 XX
 DT 12-DEC-2002 (first entry)
 DE
 DE Human HCC underexpressed gene SAGE tag #333.
 XX

KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 XX expression pattern; differential expression; ss.
 OS Homo sapiens.
 XX JP2002209591-A.
 XX PN
 XX XX
 PD 30-JUL-2002.
 XX
 XX 19-JAN-2001; 2001JP-00012328.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX PA
 XX WPI; 2002-631294/68.
 XX DR
 XX Human chronic hepatitis C tissue expression exasperating gene group
 XX PT comprises 100 high-ranking genes.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX PA
 XX WPI; 2002-631294/68.
 XX DR
 XX Human chronic hepatitis C tissue expression exasperating gene group
 XX PT comprises 100 high-ranking genes.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX Claim 28; Page 19; 139pp; Japanese.
 XX PS
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with normal liver tissue
 XX
 XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GGACTCGCT 11
 Db 2 GGACGCGCT 10
 |||||
 |||||
 RESULT 371
 ABV84764
 ID ABV84764 standard; cDNA; 10 BP.
 XX AC
 XX ABV84764;
 XX AC
 XX 12-DEC-2002 (first entry)
 XX DT
 XX Human ceruloplasmin SAGE tag #574.
 XX DE
 XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX OS
 XX Homo sapiens.
 XX PN
 XX JP2002209591-A.

PD 30-JUL-2002.
 XX
 XX 19-JAN-2001; 2001JP-00012328.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX PA
 XX WPI; 2002-631294/68.
 XX DR
 XX Human chronic hepatitis C tissue expression exasperating gene group
 XX PT comprises 100 high-ranking genes.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX Claim 46; Page 26; 139pp; Japanese.
 XX PS
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX
 XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GACTCGCTG 12
 Db 2 GACGCGCTG 10
 |||||
 |||||
 RESULT 372
 ABV84972/c
 ID ABV84972 standard; cDNA; 10 BP.
 XX AC
 XX ABV84972;
 XX AC
 XX 12-DEC-2002 (first entry)
 XX DT
 XX Human ceruloplasmin SAGE tag #782.
 XX DE
 XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.
 XX OS
 XX Homo sapiens.
 XX PN
 XX JP2002209591-A.
 XX XX
 XX 30-JUL-2002.
 XX PF
 XX 19-JAN-2001; 2001JP-00012328.
 XX PR
 XX 19-JAN-2001; 2001JP-00012328.
 XX PA
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX XX

DR	WPI; 2002-631294/68.
XX	
PT	Human chronic hepatitis C tissue expression exasperating gene group
PT	comprises 100 high-ranking genes.
XX	
PS	Claim 64; Page 31; 139pp; Japanese.
XX	
CC	The invention relates to SAGE (serial analysis of gene expression) tags
CC	representing groups of genes which are differentially expressed in human
CC	chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC	hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC	The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC	located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC	polyA region of cDNAs derived from a variety of genes. These tags serve
CC	to uniquely identify each transcript and can thus be used to analyse the
CC	pattern of gene expression in particular cell types. The invention also
CC	relates to proteins encoded by the genes expressed in chronic hepatitis C
CC	liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC	the expression of groups of genes that are overexpressed in chronic
CC	hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC	in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC	treatment of these diseases. Such genes, inhibitors of their expression
CC	or activity, and antibodies against the gene products may be used in the
CC	development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC	ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC	expressed in hepatocellular carcinoma
XX	
SQ	Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
	Query Match 37.0%; Score 7.4; DB 1; Length 10;
	Best Local Similarity 88.9%; Pred. No. 1.6e+02;
	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	11 TGGCAGCGCA 19
Db	10 TGGCAAGCA 2
RESULT 373	
ABV84741	
ID	ABV84741 standard; cDNA; 10 BP.
XX	
AC	ABV84741;
XX	
DT	12-DEC-2002 (first entry)
XX	
DE	Chronic hepatitis C/HCC differentially expressed gene SAGE tag #551.
XX	
XW	SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XW	CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XW	expression pattern; differential expression; ss.
XX	
OS	Homo sapiens.
XX	
PN	JP2002209591-A.
XX	
PD	30-JUL-2002.
XX	
PF	19-JAN-2001; 2001JP-00012328.
XX	
PR	19-JAN-2001; 2001JP-00012328.
XX	
PA	(KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX	
DR	WPI; 2002-631294/68.
XX	
XX	Human chronic hepatitis C tissue expression exasperating gene group
PT	comprises 100 high-ranking genes.
XX	
PS	Claim 46; Page 26; 139pp; Japanese.
XX	
CC	The invention relates to SAGE (serial analysis of gene expression) tags
CC	representing groups of genes which are differentially expressed in human
CC	chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC	hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC	The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC	located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC	polyA region of cDNAs derived from a variety of genes. These tags serve
CC	to uniquely identify each transcript and can thus be used to analyse the
CC	pattern of gene expression in particular cell types. The invention also
CC	relates to proteins encoded by the genes expressed in chronic hepatitis C
CC	liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC	the expression of groups of genes that are overexpressed in chronic
CC	hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC	in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC	treatment of these diseases. Such genes, inhibitors of their expression
CC	or activity, and antibodies against the gene products may be used in the
CC	development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC	ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC	expressed in hepatocellular carcinoma
XX	

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84591-ABV84790 are SAGE tags representing the 100 least highly
CC expressed genes out of those genes which are underexpressed in
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX

Seq Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
|||||
DB 2 GGACGGCT 10

RESULT 374
ABV84604
ID ABV84604 standard; cDNA; 10 BP.
XX AC ABV84604;
XX AC
XX 12-DEC-2002 (first entry)
XX Human multiple HCC/CH differentially expressed genes SAGE tag #414.
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; ss.
XX Homo sapiens.
XX JP2002209591-A.
XX 30-JUL-2002.
XX 19-JAN-2001; 2001JP-00012328.
XX 19-JAN-2001; 2001JP-00012328.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2002-631294/68.
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX Claim 37; Page 22; 139pp; Japanese.
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84591-ABV84690 are SAGE tags representing the 100 most highly
 CC expressed genes out of those genes which are overexpressed in
 CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCA 19
 |||||
 Db 2 TGGCAGGCA 10

RESULT 375
 AAS19891
 ID AAS19891 standard; DNA; 10 BP.
 XX AC AAS19891;
 XX DT 08-MAY-2002 (first entry)
 XX DE Oligonucleotide #71 to detect human RANGAP1 gene polymorphisms.
 XX KW Human; single nucleotide polymorphism; SNP; RANGAP1;
 XX KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;
 XX KW genotyping; cancer; irregular cell cycle associated disorder; primer; ss.
 XX OS Homo sapiens.
 XX PN WO200179240-A2.
 XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-US012455.
 XX PR 17-APR-2000; 2000US-0198072P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Chew A, Choi JY, Koshy B;
 XX WPI; 2002-075068/10.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
 CC genotyping the RANGAP1 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC treatment of diseases associated with RANGAP1 activity, such as cancer
 CC and other disorders associated with an irregular cell cycle. AAS19821-
 CC AAS19898 represent primer-extension oligonucleotides for detecting human
 CC RANGAP1 gene polymorphisms
 XX
 SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37.0%; Score 7.4; DB 1; Length 10;
 |||||
 Db 9 CTGGCGGC 1

Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGCTGGCAC 16
 |||||
 Db 2 CGCTGGCCC 10

RESULT 376
 AAS95980/c
 ID AAS95980 standard; DNA; 10 BP.
 XX AC AAS95980;
 XX DT 26-FEB-2002 (first entry)
 XX DE Human CALM1 gene allele-specific oligonucleotide #89.
 XX KW Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
 XX KW haplotyping; SCVA3; Alzheimer's disease; drug screening;
 XX KW calcium-dependent signal transduction; PCR primer; ss.

XX OS Homo sapiens.
 XX PN WO200179218-A2.
 XX PD 25-OCT-2001.
 XX PF 09-APR-2001; 2001WO-US011509.
 XX PR 12-APR-2000; 2000US-0196340P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
 XX WPI; 2002-049190/06.

XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
 PT expressing CALM1 protein for use in screening for candidate drugs to
 PT treat diseases related to CALM1 activity such as Alzheimer's disease.
 XX Claim 17; Page 14; 82pp; English.

XX The invention relates to an isolated polynucleotide comprising a sequence
 CC selected from a polymorphic variant of calmodulin 1 (CALM1). The
 CC polymorphic variant comprises an CALM1 isogene defined by a haplotype
 CC selected from haplotypes 1-21 given in the specification. The
 CC polymorphisms are useful for studying the biological function of CALM1 as
 CC well as in identifying drugs targeting this protein for the treatment of
 CC a disorder related to its abnormal expression or function. The
 CC polymorphic variants may also be used in screening for compounds
 CC targeting CALM1 to treat a specific condition or disease predicted to be
 CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype
 CC pair of an individual is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with SCVA3 activity, e.g. Alzheimer's
 CC disease and diseases involving defects in calcium-dependent signal
 CC transduction. Haplotyping the CALM1 gene in an individual is also useful
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease predicted to be associated with CALM1
 CC activity. AAS95982-AAS96018 represent human CALM1 allele-specific
 CC oligonucleotides and PCR primers of the invention

XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGGC 18
 |||||
 Db 9 CTGGCGGC 1

RESULT 377
 AAL39813/C
 ID AAL39813 standard; DNA; 10 BP.
 XX AC AAL39813;
 XX AC AAL39813;
 XX DT 05-SEP-2002 (first entry)
 XX DE SMOH polymorphism detecting primer SEQ ID No 128.
 XX KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;
 XX KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;
 XX KW Gene therapy; antisense gene therapy; PCR; primer; ss.
 XX OS Homo sapiens.
 XX PN WO200229004-A2.
 XX PD 11-APR-2002.
 XX PF 04-OCT-2001; 2001WO-US01304.
 XX PR 04-OCT-2000; 2000US-0237871P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;
 XX DR WPI; 2002-519113/55.
 XX PT New genetic variants of smoothened Drosophila homolog (SMOH) gene useful
 XX PT for therapeutic purposes and for expressing SMOH protein useful in
 XX PT identifying drugs to treat basal cell carcinomas.
 XX PS Claim 17; Page 16; 179pp; English.
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC which is a polymorphic variant of a reference sequence for the human
 CC smoothened Drosophila homologue (SMOH) gene or its fragment, or a
 CC polymorphic variant of a reference sequence for a SMOH cDNA or its
 CC fragment. A new isolated polypeptide is useful for screening for drugs
 CC targeting the polypeptide. A new method is useful for identifying an
 CC association between a trait such as a clinical response to a drug
 CC associating SMOH and a haplotype or haplotype pair of SMOH gene. The
 CC methods have applicability in developing diagnostic tests and therapeutic
 CC treatments for basal cell carcinomas (BCCs). The isolated polynucleotide
 CC is useful for studying the expression and function of SMOH and expressing
 CC SMOH protein for use in screening for candidate drugs to treat diseases
 CC related to SMOH activity. The polymorphism and haplotype data are useful
 CC for validating whether SMOH is a suitable target for drugs to treat BCCs,
 CC screening for the drugs and reducing bias in clinical trials of the
 CC drugs. The isolated polynucleotide is useful for therapeutic purposes.
 CC The new method, an oligonucleotide and kit of the invention are useful
 CC for determining whether an individual has one of the haplotypes or the
 CC haplotype pairs. The polynucleotides of the invention can be used to
 CC treat disorders by gene therapy and antisense gene therapy. This
 CC polynucleotide sequence represents a primer used for detecting human
 CC smoothened Drosophila homologue gene polymorphisms of the invention
 XX SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TCGCTGGCA 15
 |||||
 Db 9 TCCCTGGCA 1

RESULT 378

ACA94531
 ID ACA94531 standard; DNA; 10 BP.
 XX AC ACA94531;
 XX AC ACA94531;
 XX DT 18-JUL-2003 (first entry)
 XX DE DNA tag from human transcript repressed in adenomas/cancers #64.
 XX KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 XX KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 XX KW kidney proximal tubule.
 XX OS Homo sapiens.
 XX PN WO2003022863-A1.
 XX PD 20-MAR-2003.
 XX PF 09-SEP-2002; 2002WO-US028518.
 XX PR 07-SEP-2001; 2001US-0317494P.
 XX PR 30-MAY-2002; 2002US-0383805P.
 XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PI Buckhaults P, Kinzler KW, Vogelstein B;
 XX DR WPI; 2003-313220/30.
 XX PT Detecting colorectal cancer in a subject, involves detecting macrophage
 XX PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 XX PT of the subject.
 XX PS Disclosure; Page 28; 59pp; English.
 CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCA 19
 |||||
 Db 2 TGGCAGCA 10

RESULT 379
 ACA94571
 ID ACA94571 standard; DNA; 10 BP.
 AC ACA94571;
 XX
 XX 18-JUL-2003 (first entry)
 DT
 DE DNA tag from human transcript repressed in adenomas/cancers #104.
 XX
 KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 PN WO2003022863-A1.
 XX
 PD 20-MAR-2003.
 XX
 XX 09-SEP-2002; 2002WO-US028518.
 PF
 XX 07-SEP-2001; 2001US-0317494P.
 PR
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 XX (UWJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Buckhaults P, Kinzler KW, Vogelstein B;
 XX WPI; 2003-313220/30.
 DR
 XX
 PT Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 PS Disclosure; Page 29; 59pp; English.

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC the subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a

CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
 |||||
 Db 2 GGACTCACT 10

RESULT 380
 ACA94570
 ID ACA94570 standard; DNA; 10 BP.
 AC ACA94570;
 XX
 XX 18-JUL-2003 (first entry)
 DT
 DE DNA tag from human transcript repressed in adenomas/cancers #103.
 XX
 KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 PN WO2003022863-A1.
 XX
 PD 20-MAR-2003.
 XX
 XX 09-SEP-2002; 2002WO-US028518.
 PF
 XX 07-SEP-2001; 2001US-0317494P.
 PR
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 XX (UWJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Buckhaults P, Kinzler KW, Vogelstein B;
 XX WPI; 2003-313220/30.
 DR
 XX
 PT Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 PS Disclosure; Page 29; 59pp; English.

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC the subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a

CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCT 11
 |||||
 Db 2 GGACTCACT 10

RESULT 381
 ADA62596/c
 ID ADA62596 standard; DNA; 10 BP.

AC ADA62596;
 XX
 DT 20-NOV-2003 (first entry)
 DE Zinc finger target sequence DNA #233.
 XX ds; target sequence; zinc finger protein;
 XX multi-finger zinc finger protein; improved affinity;
 XX improved specificity; enhanced biological activity.

OS Synthetic.

XX US2003068675-A1.

XX 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.
 XX 24-MAR-1999; 99US-0126239P.
 XX 30-JUL-1999; 99US-0146595P.
 XX 30-JUL-1999; 99US-0146615P.
 XX 23-MAR-2000; 2000US-00535008.
 XX 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX Liu Q;

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus
 XX and C-terminus that bind to subsites in 3' to 5' direction, in a target
 XX site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 17; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The
 XX method is useful for designing a zinc finger protein. The method provides
 XX multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The
 CC present sequence represents a zinc finger protein DNA target sequence.

SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
 |||||
 Db 9 CGCTGCCAC 1

RESULT 382
 ADA62597/c
 ID ADA62597 standard; DNA; 10 BP.

XX ADA62597;

XX 20-NOV-2003 (first entry)

XX Zinc finger target sequence DNA #234.

XX ds; target sequence; zinc finger protein;
 XX multi-finger zinc finger protein; improved affinity;
 XX improved specificity; enhanced biological activity.

OS Synthetic.

XX US2003068675-A1.

XX 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

XX 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

XX 30-JUL-1999; 99US-0146595P.

XX 30-JUL-1999; 99US-0146615P.

XX 23-MAR-2000; 2000US-00535008.

XX 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

XX Liu Q;

XX WPI; 2003-567233/53.

XX Designing zinc finger protein that has three zinc fingers from N-terminus
 XX and C-terminus that bind to subsites in 3' to 5' direction, in a target
 XX site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 17; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The
 XX method is useful for designing a zinc finger protein. The method provides
 XX multi-finger zinc finger proteins with improved affinity and specificity
 XX for their target sequences, as well as enhanced biological activity. The
 XX present sequence represents a zinc finger protein DNA target sequence.

SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16
 |||||
 Db 9 CGCTGCCAC 1

RESULT 383


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ADCI1772
ID  ADKI1772 standard; DNA; 10 BP.
XX
XX  AC  ADKI1772;
XX
XX  AC  ADKI1772;
XX
XX  DT  18-DEC-2003 (first entry)
XX
XX  DE  Monobactam related tethered diene SEQ ID NO:22.
XX
XX  SS; monobactam; antibacterial; PBP2a; inhibitor;
XX  methicillin resistant Staphylococcus aureus; MRSA; lactam antibiotic.
XX
XX  OS  Synthetic.
XX
XX  PN  WO2003051314-A2.
XX
XX  PD  26-JUN-2003.
XX
XX  PF  18-DEC-2002; 2002WO-US040739.
XX
XX  PR  18-DEC-2001; 2001US-0340255P.
XX
XX  PA  (INVE-) INVENUX INC.
XX
XX  PI  Eaton B, Tarasow T, Nieuwlandt D, Dewey T;
XX  WPI; 2003-618003/58.
XX
XX  DR  New monobactam compounds used as antibacterial agents against e.g.
XX  PT  methicillin resistant Staphylococcus aureus.
XX
XX  Example 6; SEQ ID NO 22; 64pp; English.
XX
XX  CC  The invention relates to novel monobactam compounds. A compound of the
XX  invention has antibacterial activity, and acts as a PBP2a inhibitor. The
XX  compounds are used as antibacterial agents. The monobactam compounds
XX  restore sensitivity of methicillin resistant Staphylococcus aureus to
XX  lactam antibiotic by targeting the molecular mechanism of resistance. The
XX  present sequence is used in the exemplification of the invention.
XX
XX  SQ  Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CTGGCAGCG 18
DB      2 CAGGCGCG 10

RESULT 384
ADD71264/c
ID  ADD71264 standard; DNA; 10 BP.
XX
XX  AC  ADD71264;
XX
XX  DT  15-JAN-2004 (first entry)
XX
XX  DE  Mouse ET gene 3' splice acceptor site from intron 4.
XX
XX  KW  Mouse; ethenolaminephosphate cytidyl transferase; ET; ds;
XX  splice acceptor site; antilipemic; cardiant; anorectic;
XX  phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
XX  cardiovascular disease; atherosclerosis; obesity.
XX
XX  OS  Mus musculus.
XX
XX  PN  US2003194795-A1.
XX
XX  PD  16-OCT-2003.
XX
XX  PF  21-MAR-2002; 2002US-00101957.

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XX
XX  PR  21-MAR-2002; 2002US-00101957.
XX
XX  PA  (BAKO/) BAKOVIC M.
XX  (POLO/) POLOUMIENKO A.
XX
XX  PI  Bakovic M, Poloumienko A;
XX
XX  DR  WPI; 2003-844457/78.
XX
XX  SS  New gene encoding a protein having ethanolaninephosphate
XX  cytidyltransferase activity, useful for treating Zellweger's syndrome, or
XX  lipid-related diseases such as cardiovascular diseases and obesity.
XX
XX  Example 1; Page 6; 22pp; English.
XX
XX  CC  The invention relates to a mouse gene encoding a protein having
XX  ethanolaninephosphate cytidyltransferase (ET) activity appearing as
XX  ADD71226, a degenerate variant of the ET gene, or a sequence that
XX  hybridises to the complement of the ET gene under stringent conditions.
XX  Also included is a promoter of a human ethanolaninephosphate
XX  cytidyltransferase gene appearing as ADD71227. The gene and promoter are
XX  useful for producing a transgenic animal, and for identifying,
XX  preventing, and treating diseases (by gene therapy) related to
XX  inappropriate phosphatidylethanolamine production, e.g. Zellweger's
XX  syndrome, or lipid-related diseases such as cardiovascular diseases,
XX  atherosclerosis and obesity. The present sequence is a mouse ET gene 3'
XX  splice acceptor site.
XX
XX  SQ  Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ACTGCTGG 13
DB      10 ACTGCTGG 2

RESULT 385
AAZ18667/c
ID  AAZ18667 standard; DNA; 11 BP.
XX
XX  AC  AAZ18667;
XX
XX  DT  22-OCT-1999 (first entry)
XX
XX  DE  Murine MRL SAGE tag 1395020.
XX
XX  KW  Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
XX  healing response; microsatellite marker; treatment; central nerve;
XX  peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX  OS  Mus sp.
XX
XX  PN  WO9941364-A2.
XX
XX  PD  19-AUG-1999.
XX
XX  PF  12-FEB-1999; 99WO-US002962.
XX
XX  PR  13-FEB-1998; 98US-0074737P.
XX  26-AUG-1998; 98US-0097937P.
XX  28-SEP-1998; 98US-0102051P.
XX
XX  PA  (WIST-) WISTAR INST.
XX
XX  PI  Heber-Katz E;
XX
XX  DR  WPI; 1999-494533/41.
XX
XX  PF  New mammalian model for enhanced wound healing - useful for identifying

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PT enhanced wound healing genes.
 PS Claim 13; Page 71; 136pp; English.
 XX
 CC This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AA218691-219036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 ACTCGCTGG 13
 DB 11 ACTGGCTGG 3
 RESULT 386
 AA218779
 ID AA218779 standard; DNA; 11 BP.
 AC AA218779;
 XX
 DT 22-OCT-1999 (first entry)
 DE Murine C57BL/6 SAGE tag 501674.
 KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
 XX
 OS Mus sp.
 XX
 PN WO9941364-A2.
 XX
 PD 19-AUG-1999.
 XX
 PF 12-FEB-1999; 99WO-US002962.
 XX
 PR 13-FEB-1998; 98US-0074737P.
 PR 26-AUG-1998; 98US-0097937P.
 PR 28-SEP-1998; 98US-0102051P.
 XX
 PA (WIST-) WISTAR INST.
 XX
 PI Heber-Katz E;
 XX
 DR WPI; 1999-494533/41.
 XX
 PT New mammalian model for enhanced wound healing - useful for identifying
 XX enhanced wound healing genes.
 PS Claim 13; Page 57; 136pp; English.
 XX
 CC This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the

CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AA218691-219036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 ACTCGCTGG 13
 DB 1 ACTGGCTGG 9
 RESULT 387
 ABQ87660
 ID ABQ87660 standard; cDNA; 11 BP.
 XX
 AC ABQ87660;
 XX
 DT 10-SEP-2002 (first entry)
 DE Human skin stress/ageing related EST SEQ ID NO 1415.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 XX screening for cosmetic or therapeutic agents, based on differential gene
 XX expression.
 XX
 PS Claim 8; Page 97; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention

XX
SQ Sequence 11 BP; 0 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CGCTGGCAC 16
Dbb 3 CGCTGGCCC 11
RESULT 388
ABQ87184
ID ABQ87184 standard; cDNA; 11 BP.
XX
AC ABQ87184;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 939.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
FN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
screening for cosmetic or therapeutic agents, based on differential gene
expression.
XX
PS Claim 8; Page 76; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
or animals, are important for skin ageing and/or skin stress by serial
analysis of gene expression between mixtures of transcribed and
optionally translated, genetically encoded factors (A) obtained from
young and aged skin, to identify that genes that show strong differential
expression. (A) comprises protein or mRNAs or their fragments. (M1) is
useful for: identifying markers of skin ageing and/or stress; determining
skin ageing and/or stress; and identifying or determining the effects of
pharmaceutical or cosmetic agents for control of skin ageing. The present
sequence is one of a group of human skin ageing/stress related expressed
sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CTGCTGGC 14
Dbb 2 CTGCTGGC 10
RESULT 389
ABQ86321
ID ABQ86321 standard; cDNA; 11 BP.
XX

AC ABQ86321;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 76.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
FN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
screening for cosmetic or therapeutic agents, based on differential gene
expression.
XX
PS Claim 8; Page 40; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
or animals, are important for skin ageing and/or skin stress by serial
analysis of gene expression between mixtures of transcribed and
optionally translated, genetically encoded factors (A) obtained from
young and aged skin, to identify that genes that show strong differential
expression. (A) comprises protein or mRNAs or their fragments. (M1) is
useful for: identifying markers of skin ageing and/or stress; determining
skin ageing and/or stress; and identifying or determining the effects of
pharmaceutical or cosmetic agents for control of skin ageing. The present
sequence is one of a group of human skin ageing/stress related expressed
sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 CTGGCACGC 18
Dbb 2 CAGGCACGC 10
RESULT 390
ABQ87581/c
ID ABQ87581 standard; cDNA; 11 BP.
XX
AC ABQ87581;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 1336.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
FN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX

PR 03-JAN-2001; 2001DE-01000121.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-528865/56.
 DR Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX Claim 8; Page 94; 325pp; German.
 XX The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGCTGGCAC 16
 DB 10 CACTGGCAC 2
 RESULT 391
 ABV64284/C
 ID ABV64284 standard; cDNA; 11 BP.
 XX AC ABV64284;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 2070.
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 82; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGGACTGCG 10
 DB 9 TGGACTGCG 1
 RESULT 392
 ABV68538
 ID ABV68538 standard; cDNA; 11 BP.
 XX AC ABV68538;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 6324.
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 201; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX

SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCTG 12
 |||||
 Db 1 GACTCTCTG 9

RESULT 393
 ABV70252
 ID ABV70252 standard; cDNA; 11 BP.
 AC ABV70252;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 8038.
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 228; 1345pp; German.
 PS The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGCG 14
 |||||
 Db 2 CTGGCTGCG 10

RESULT 395
 ABV66405/c
 ID ABV66405 standard; cDNA; 11 BP.
 AC ABV66405;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 4191.
 DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS

CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (BST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 TGGACTGCG 10
 Db 9 TGGACTGCG 1
 RESULT 398
 ABV65118/c
 ID ABV65118 standard; cDNA; 11 BP.
 XX
 AC ABV65118;
 XX
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 2904.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 105; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (BST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 CTCGCTGGC 14
 Db 10 CTCGCTGGC 2
 RESULT 399
 ABV68885
 ID ABV68885 standard; cDNA; 11 BP.
 XX
 AC ABV68885;
 XX
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 6671.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 210; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (BST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ATGGAATCG 9
 Db 2 ACGGACTCG 10
 RESULT 400
 ABV65480/c
 ID ABV65480 standard; cDNA; 11 BP.
 XX
 AC ABV65480;
 XX
 DT 21-OCT-2002 (first entry)

XX DE Human skin EST 3266.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 115; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACTGCTGG 13
||| ||||
DB 11 ACTGCTGG 3
RESULT 401
ABV62831
ID ABV62831 standard; cdNA; 11 BP.
XX AC ABV62831;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 617.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.

PF 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 42; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 GGCACGCAC 20
||||| |||
DB 3 GGCACACAC 11
RESULT 402
ABV63636/C
ID ABV63636 standard; cdNA; 11 BP.
XX AC ABV63636;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 1422.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.

XX PS Disclosure; Page 64; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed

XX CC in the skin of humans or animals by subjecting a mixture of genetically

XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)

XX CC so as to identify skin-expressed genes and quantify their expression.

XX CC (M1) is useful for identifying genes involved in skin homeostasis; to

XX CC determine skin homeostasis and to test agent (A) that maintains or

XX CC promotes skin homeostasis or that can be used for treating skin

XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

XX CC skin. The present sequence is that of a human expressed sequence tag

XX CC (EST) of the invention

XX SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20

Db 9 GGCACGCAC 1

RESULT 403

ABV67898/c

ID ABV67898 standard; cDNA; 11 BP.

XX AC ABV67898;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 5684.

XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;

XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX DR WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining

XX PT homeostasis and identifying cosmetic or pharmaceutical agents against

XX PT e.g. skin cancer.

XX PS Disclosure; Page 182; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed

XX CC in the skin of humans or animals by subjecting a mixture of genetically

XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)

XX CC so as to identify skin-expressed genes and quantify their expression.

XX CC (M1) is useful for identifying genes involved in skin homeostasis; to

XX CC determine skin homeostasis and to test agent (A) that maintains or

XX CC promotes skin homeostasis or that can be used for treating skin

XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

XX CC skin. The present sequence is that of a human expressed sequence tag

XX CC (EST) of the invention

XX SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20

Db 11 GGCACCCAC 3

RESULT 404

ABV69858/c

ID ABV69858 standard; cDNA; 11 BP.

XX AC ABV69858;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 7644.

XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;

XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX DR WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining

XX PT homeostasis and identifying cosmetic or pharmaceutical agents against

XX PT e.g. skin cancer.

XX PS Claim 24; Page 242; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed

XX CC in the skin of humans or animals by subjecting a mixture of genetically

XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)

XX CC so as to identify skin-expressed genes and quantify their expression.

XX CC (M1) is useful for identifying genes involved in skin homeostasis; to

XX CC determine skin homeostasis and to test agent (A) that maintains or

XX CC promotes skin homeostasis or that can be used for treating skin

XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

XX CC skin. The present sequence is that of a human expressed sequence tag

XX CC (EST) of the invention

XX SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTGCTGG 13

Db 9 ACTAGCTGG 1

```

RESULT 405
ABV69088
ID ABV69088 standard; cDNA; 11 BP.
XX
XX
AC ABV69088;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 6874.
XX
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EF015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 216; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 37.0%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 11 TGCCACGCA 19
Db 2 TGCCCGCA 10
|||||
|||||

RESULT 406
ABV65801
ID ABV65801 standard; cDNA; 11 BP.
XX
XX
AC ABV65801;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 3587.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX

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KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EF015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 124; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 37.0%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 10 CTGGCAGCGC 18
Db 2 CAGGCAGCGC 10
|||||
|||||

RESULT 407
ABV67499
ID ABV67499 standard; cDNA; 11 BP.
XX
XX
AC ABV67499;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 5285.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EF015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX

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XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 171; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCCTGGCA 15
DB 1 TCCTGGCA 9
||| |||||

RESULT 408
ABV71057/c
ID ABV71057 standard; cDNA; 11 BP.
XX
XX ABV71057;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 8843.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Claim 24; Page 284; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically

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CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
DB 9 GGCACGCAC 1
||||| |||

RESULT 409
ABV67744/c
ID ABV67744 standard; cDNA; 11 BP.
XX
XX ABV67744;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 5530.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 177; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

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XX PD 11-JUL-2002.
 XX XX
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX XX
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX XX
 XX PA (HENK) HENKEL KGAA.
 XX XX
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX XX
 XX PT In vitro identification of skin-expressed genes, useful for determining
 XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
 XX PT e.g. skin cancer.
 XX XX
 XX PS Disclosure; Page 218; 1345pp; German.
 XX XX
 XX CC The invention relates to in vitro identification (MI) of genes expressed
 XX CC in the skin of humans or animals by subjecting a mixture of genetically
 XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 XX CC so as to identify skin-expressed genes and quantify their expression.
 XX CC (MI) is useful for identifying genes involved in skin homeostasis; to
 XX CC determine skin homeostasis and to test agent (A) that maintains or
 XX CC promotes skin homeostasis or that can be used for treating skin
 XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 XX CC skin. The present sequence is that of a human expressed sequence tag
 XX CC (EST) of the invention
 XX SQ Sequence 11 BP; 4 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GGCAGCGCAC 20
 Db 1 GGCAGCGCAC 9
 |||||
 |||||
 RESULT 413
 ABL91911
 ID ABL91911 standard; cDNA; 11 BP.
 AC ABL91911;
 XX XX
 XX DT 30-MAY-2002 (first entry)
 XX XX
 XX DE Human Pan-Endothelial Marker SEQ ID NO 9.
 XX XX
 XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 XX KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 XX KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 XX KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 XX KW psoriasis; ss.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200210217-A2.
 XX XX
 XX PD 07-FEB-2002.
 XX XX
 XX PF 01-AUG-2001; 2001WO-US024031.
 XX XX
 XX PR 02-AUG-2000; 2000US-0222599P.
 XX PR 11-AUG-2000; 2000US-0224360P.
 XX PR 11-APR-2001; 2001US-0282850P.
 XX XX
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX XX
 XX CC

PI St Croix B, Kinzler KW, Vogelstein B;
 XX WPI; 2002-291856/33.
 XX XX
 XX PT An isolated molecule comprising an antibody variable region which
 XX PT specifically binds to an extracellular domain of a tumor endothelial
 XX PT marker (TEM) protein, useful for inhibiting tumor growth.
 XX XX
 XX PS Example 4; Page 324; 33pp; English.
 XX XX
 XX CC The invention relates to an isolated molecule comprising an antibody
 XX CC variable region which specifically binds to an extracellular domain of a
 XX CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 XX CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 XX CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 XX CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
 XX CC bearing a vascularised tumour, polycystic kidney disease, diabetic
 XX CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
 XX CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90769)
 XX CC are disclosed, as are marker oligonucleotide sequences: tumour
 XX CC endothelial markers (TEM) ABL91936-ABL92041 and ABL92143-ABL92191; normal
 XX CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 XX CC (PEM) ABL91903-ABL91995. The present sequence is that of an
 XX CC oligonucleotide marker useful to the invention
 XX SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TCGCTGGCA 15
 Db 1 TCCCTGGCA 9
 |||||
 |||||
 RESULT 414
 AAD27543/c
 ID AAD27543 standard; DNA; 11 BP.
 XX XX
 XX AC AAD27543;
 XX XX
 XX DT 18-APR-2002 (first entry)
 XX XX
 XX DE pGL3 basic vector CCCGG motif 5' flanking DNA.
 XX XX
 XX KW p53 protein; pGL3 luciferase reporter vector; luc+; transcription factor;
 XX KW cell cycle control; DNA damage repair; pGL3 basic vector; apoptosis; ds.
 XX OS Unidentified.
 XX XX
 XX PN WO200196602-A2.
 XX XX
 XX PD 20-DEC-2001.
 XX XX
 XX PF 18-JUN-2001; 2001WO-GB002718.
 XX XX
 XX PR 16-JUN-2000; 2000GB-00014820.
 XX XX
 XX PA (MEDI-) MEDICAL RES COUNCIL.
 XX PI Yang AL, Festing M;
 XX DR WPI; 2002-130743/17.
 XX XX
 XX PT Determining the p53 status of a sample, useful for assaying for mimetics
 XX PT or antagonists of p53, or for the presence of DNA damage, comprises
 XX PT determining whether p53 binds to the pGL3 vector in a sample containing a
 XX PT pGL3 vector.
 XX PS Disclosure; Page 12; 53pp; English.
 XX XX
 XX CC The patent discloses methods for determining the p53 status of a sample

CC which comprise providing a sample containing a pGL3 luciferase reporter
CC vector and determining whether p53 binds to the pGL3 vector. p53 is a
CC transcription factor that regulates many genes including those associated
CC with cell cycle control, apoptosis and DNA damage repair. pGL3 reporter
CC vectors contain a modified firefly luciferase cDNA designated luc+. p53
CC protein binds to pGL3-basic vector and causes luciferase expression. The
CC method is useful for determining the p53 status of a sample. It is also
CC useful for assaying for mimetics or antagonists of p53 and for assaying
CC for presence of activated p53 and/or DNA damage. The invention also
CC relates to a method of modifying pGL3 vector which involves deletion or
CC alteration of a CCCGGG motif of the pGL3 vector and/or deleting or
CC altering a sequence within 20 bp sequence 5' or 3' of CCCGGG motif. The
CC nucleic acid having a sequence incorporating the CCCGGG motif is useful
CC for conferring promoter activity or p53-responsiveness on a nucleic acid
CC encoding a polypeptide of interest or in assays for p53 transcriptional
CC activity. The present DNA sequence is pGL3 basic vector CCCGGG motif 5',
CC flanking DNA. This sequence is used along with CCCGGG motif to confer
CC promoter activity
XX
XX
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCG 18
Db 11 CTAGCAGCG 3

RESULT 415
ABX71836
ID ABX71836 standard; DNA; 11 BP.
XX
AC ABX71836;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA tag used to identify human gene encoding PEM 9.
XX
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neoangiogenesis; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS Homo sapiens.
XX
PN WO200283874-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US008253.
XX
PR 11-APR-2001; 2001US-0282850P.
PR 06-FEB-2002; 2002US-0354262P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
DR
XX
XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; Page 89; 374pp; English.
XX
CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in

CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC represent DNA tags for human PEM, TEM or NEM genes
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCGCTGGCA 15
Db 1 TCCTGGCA 9

Search completed: June 8, 2004, 12:25:35
Job time : 2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 12:21:50 ; Search time 0.001 Seconds

(without alignments)
141.480 Million cell updates/sec

Title: US-10-003-919-21

Perfect score: 20

Sequence: 1 ATGGACTCGTGGCAGCAC 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 317 seqs, 3537 residues

Total number of hits satisfying chosen parameters: 634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 318 summaries

Database : rgddb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	67.0	20	1	ACCESSION:AX292886
C 2	13.2	66.0	20	1	ACCESSION:AR211959
C 3	13	65.0	18	1	ACCESSION:AR098804
C 4	11.2	56.0	17	1	ACCESSION:AR074734
C 5	11	55.0	17	1	ACCESSION:AR074734
C 6	10.4	52.0	12	1	ACCESSION:AX350138
C 7	10.4	52.0	15	1	ACCESSION:AR180569
C 8	10.4	52.0	16	1	ACCESSION:AR328418
C 9	10.4	52.0	16	1	ACCESSION:AX268358
C 10	10.2	51.0	15	1	ACCESSION:AR125055
C 11	10.2	51.0	15	1	ACCESSION:AR285771
C 12	10.2	51.0	15	1	ACCESSION:AR397762
C 13	10	50.0	11	1	ACCESSION:AX624655
C 14	10	50.0	11	1	ACCESSION:AX632076
C 15	10	50.0	15	1	BD005894
C 16	9.8	49.0	15	1	ACCESSION:AR175758
C 17	9.8	49.0	15	1	ACCESSION:E13070
C 18	9.8	49.0	15	1	ACCESSION:E14044
C 19	9.8	49.0	15	1	ACCESSION:E15462
C 20	9.8	49.0	15	1	ACCESSION:AR193001
C 21	9.8	49.0	15	1	AR326741
C 22	9.8	49.0	15	1	ACCESSION:AX698541
C 23	9.8	49.0	15	1	BD141542
C 24	9.8	49.0	15	1	BD176038
C 25	9.4	47.0	11	1	ACCESSION:AX624728
C 26	9.4	47.0	11	1	ACCESSION:AX632149
C 27	9.4	47.0	12	1	ACCESSION:AR1521
C 28	9.4	47.0	14	1	ACCESSION:AR349598
C 29	9.4	47.0	14	1	BD225400
C 30	9	45.0	10	1	BD239415
C 31	9	45.0	10	1	BD23954
C 32	9	45.0	10	1	BD23954
C 33	9	45.0	11	1	ACCESSION:AX153274
					ACCESSION:AX624613

34	9	45.0	11	1	AX625787
35	9	45.0	11	1	AX632034
36	9	45.0	12	1	AR135801
37	9	45.0	12	1	AR135802
38	9	45.0	13	1	AR094449
39	9	45.0	13	1	AR154534
40	9	45.0	13	1	AR175358
41	9	45.0	13	1	AR362035
42	9	45.0	13	1	AR362037
43	9	45.0	13	1	AR362041
44	9	45.0	13	1	AR362043
45	9	45.0	13	1	AR362049
46	9	45.0	13	1	AR362051
47	9	45.0	13	1	AX078151
48	9	45.0	13	1	AX078153
49	9	45.0	13	1	AX078157
50	9	45.0	13	1	AX078159
51	9	45.0	13	1	AX078165
52	9	45.0	13	1	AX078167
53	9	45.0	13	1	BD209805
54	9	45.0	13	1	BD209807
55	9	45.0	13	1	BD209811
56	9	45.0	13	1	BD209813
57	9	45.0	13	1	BD209819
58	9	45.0	13	1	BD209821
59	8.8	44.0	12	1	AR034976
60	8.8	44.0	12	1	AR034978
61	8.8	44.0	12	1	AR082060
62	8.8	44.0	12	1	AR082062
63	8.8	44.0	12	1	AR118451
64	8.8	44.0	12	1	AR118453
65	8.8	44.0	12	1	AR151019
66	8.8	44.0	12	1	AR151021
67	8.8	44.0	12	1	AR199166
68	8.8	44.0	12	1	AR199168
69	8.8	44.0	12	1	AR218175
70	8.8	44.0	12	1	AR218177
71	8.8	44.0	12	1	AR222615
72	8.8	44.0	12	1	AR222617
73	8.8	44.0	12	1	AR231653
74	8.8	44.0	12	1	BD231655
75	8.4	42.0	10	1	BD231655
76	8.4	42.0	10	1	BD238599
77	8.4	42.0	10	1	BD239966
78	8.4	42.0	10	1	E54650
79	8.4	42.0	10	1	AX152491
80	8.4	42.0	10	1	AX301297
81	8.4	42.0	10	1	BD166770
82	8.4	42.0	10	1	BD166807
83	8.4	42.0	10	1	BD166975
84	8.4	42.0	10	1	BD167022
85	8.4	42.0	10	1	BD167056
86	8.4	42.0	10	1	BD167184
87	8.4	42.0	11	1	AX470770
88	8.4	42.0	11	1	AX471056
89	8.4	42.0	11	1	AX471099
90	8.4	42.0	11	1	AX471193
91	8.4	42.0	11	1	AX471729
92	8.4	42.0	11	1	AX623912
93	8.4	42.0	11	1	AX624033
94	8.4	42.0	11	1	AX624211
95	8.4	42.0	11	1	AX624372
96	8.4	42.0	11	1	AX624551
97	8.4	42.0	11	1	AX626287
98	8.4	42.0	11	1	AX626311
99	8.4	42.0	11	1	AX629490
100	8.4	42.0	11	1	AX629976
101	8.4	42.0	11	1	AX631333
102	8.4	42.0	11	1	AX631454
103	8.4	42.0	11	1	AX631632
104	8.4	42.0	11	1	AX631793
105	8.4	42.0	11	1	AX631972
106	8.4	42.0	12	1	BD091223
					BD234977

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ACCESSION:AX632034
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ACCESSION:AR135802
ACCESSION:AR094449
ACCESSION:AR154534
ACCESSION:AR175358
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ACCESSION:AR362037
ACCESSION:AR362041
ACCESSION:AR362043
ACCESSION:AR362049
ACCESSION:AR362051
ACCESSION:AX078151
ACCESSION:AX078153
ACCESSION:AX078157
ACCESSION:AX078159
ACCESSION:AX078165
ACCESSION:AX078167
ACCESSION:BD209805
ACCESSION:BD209807
ACCESSION:BD209811
ACCESSION:BD209813
ACCESSION:BD209819
ACCESSION:BD209821
ACCESSION:AR034976
ACCESSION:AR034978
ACCESSION:AR082060
ACCESSION:AR082062
ACCESSION:AR118451
ACCESSION:AR118453
ACCESSION:AR151019
ACCESSION:AR151021
ACCESSION:AR199166
ACCESSION:AR199168
ACCESSION:AR218175
ACCESSION:AR218177
ACCESSION:AR222615
ACCESSION:AR222617
ACCESSION:AR231653
ACCESSION:BD231655
ACCESSION:BD238599
ACCESSION:BD239966
ACCESSION:E54650
ACCESSION:AX152491
ACCESSION:AX301297
ACCESSION:BD166770
ACCESSION:BD166807
ACCESSION:BD166975
ACCESSION:BD167022
ACCESSION:BD167056
ACCESSION:BD167184
ACCESSION:AX470770
ACCESSION:AX471056
ACCESSION:AX471099
ACCESSION:AX471193
ACCESSION:AX471729
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ACCESSION:AX624033
ACCESSION:AX624211
ACCESSION:AX624372
ACCESSION:AX624551
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ACCESSION:AX629490
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ACCESSION:AX631333
ACCESSION:AX631454
ACCESSION:AX631632
ACCESSION:AX631793
ACCESSION:AX631972
BD091223
BD234977

C 107	8.4	42.0	12	1	AX009048	ACCESSION:AX009048	180	7.8	39.0	12	1	AR100990	ACCESSION:AR100990
C 108	8	40.0	9	1	AX767991	ACCESSION:AX767991	181	7.8	39.0	12	1	AR100991	ACCESSION:AR100991
C 109	8	40.0	10	1	AS2274	ACCESSION:AS2274	182	7.8	39.0	12	1	AR167817	ACCESSION:AR167817
C 110	8	40.0	10	1	AS1804	ACCESSION:AS1804	183	7.8	39.0	12	1	E29701	ACCESSION:E29701
C 111	8	40.0	10	1	A97598	ACCESSION:A97598	184	7.8	39.0	12	1	E38807	ACCESSION:E38807
C 112	8	40.0	10	1	AR016246	ACCESSION:AR016246	185	7.8	39.0	12	1	E64233	ACCESSION:E64233
C 113	8	40.0	10	1	AR044027	ACCESSION:AR044027	186	7.8	39.0	12	1	AR199084	ACCESSION:AR199084
C 114	8	40.0	10	1	AR079092	ACCESSION:AR079092	187	7.8	39.0	12	1	AR371423	ACCESSION:AR371423
C 115	8	40.0	10	1	AR079528	ACCESSION:AR079528	188	7.8	39.0	12	1	AR371424	ACCESSION:AR371424
C 116	8	40.0	10	1	AR099718	ACCESSION:AR099718	189	7.8	39.0	12	1	AX098966	ACCESSION:AX098966
C 117	8	40.0	10	1	AR113051	ACCESSION:AR113051	C 189	7.8	39.0	12	1	AX136991	ACCESSION:AX136991
C 118	8	40.0	10	1	AR167221	ACCESSION:AR167221	C 190	7.8	39.0	12	1	AX350140	ACCESSION:AX350140
C 119	8	40.0	10	1	B0239869	ACCESSION:BD239869	C 191	7.8	39.0	12	1	AX350140	ACCESSION:AX350140
C 120	8	40.0	10	1	BD240506	ACCESSION:BD240506	192	7.8	39.0	12	1	AX698726	ACCESSION:AX698726
C 121	8	40.0	10	1	BD248338	ACCESSION:BD248338	193	7.8	39.0	12	1	BD105403	ACCESSION:BD105403
C 122	8	40.0	10	1	I22447	ACCESSION:I22447	194	7.8	39.0	12	1	BD105404	ACCESSION:BD105404
C 123	8	40.0	10	1	I34793	ACCESSION:I34793	195	7.8	39.0	12	1	BD105407	ACCESSION:BD105407
C 124	8	40.0	10	1	I64511	ACCESSION:I64511	196	7.4	37.0	9	1	AX668767	ACCESSION:AX668767
C 125	8	40.0	10	1	AR238724	ACCESSION:AR238724	197	7.4	37.0	9	1	AX668837	ACCESSION:AX668837
C 126	8	40.0	10	1	AR270938	ACCESSION:AR270938	198	7.4	37.0	9	1	AX668837	ACCESSION:AX668837
C 127	8	40.0	10	1	AX016299	ACCESSION:AX016299	199	7.4	37.0	9	1	AR000035	ACCESSION:AR000035
C 128	8	40.0	10	1	AX152168	ACCESSION:AX152168	200	7.4	37.0	10	1	AR020450	ACCESSION:AR020450
C 129	8	40.0	10	1	BD023238	ACCESSION:BD023238	201	7.4	37.0	10	1	AR028150	ACCESSION:AR028150
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C 131	8	40.0	10	1	BD107610	ACCESSION:BD107610	C 203	7.4	37.0	10	1	AR081130	ACCESSION:AR081130
C 132	8	40.0	11	1	AR023571	ACCESSION:AR023571	C 204	7.4	37.0	10	1	AR085327	ACCESSION:AR085327
C 133	8	40.0	11	1	AR082679	ACCESSION:AR082679	C 205	7.4	37.0	10	1	AR088075	ACCESSION:AR088075
C 134	8	40.0	11	1	AX156206	ACCESSION:AR156206	C 206	7.4	37.0	10	1	AR104234	ACCESSION:AR104234
C 135	8	40.0	11	1	AR301731	ACCESSION:AR301731	C 207	7.4	37.0	10	1	AR143498	ACCESSION:AR143498
C 136	8	40.0	11	1	AX381088	ACCESSION:AR381088	208	7.4	37.0	10	1	BD238715	ACCESSION:BD238715
C 137	8	40.0	11	1	AX470788	ACCESSION:AX470788	C 209	7.4	37.0	10	1	BD239057	ACCESSION:BD239057
C 138	8	40.0	11	1	AX471274	ACCESSION:AX471274	210	7.4	37.0	10	1	BD239061	ACCESSION:BD239061
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C 142	8	40.0	11	1	AX624914	ACCESSION:AX624914	214	7.4	37.0	10	1	BD270828	ACCESSION:BD270828
C 143	8	40.0	11	1	AX625058	ACCESSION:AX625058	C 215	7.4	37.0	10	1	I86912	ACCESSION:I86912
C 144	8	40.0	11	1	AX625700	ACCESSION:AX625700	216	7.4	37.0	10	1	I89787	ACCESSION:I89787
C 145	8	40.0	11	1	AX625812	ACCESSION:AX625812	217	7.4	37.0	10	1	I90091	ACCESSION:I90091
C 146	8	40.0	11	1	AX628487	ACCESSION:AX628487	218	7.4	37.0	10	1	AR205452	ACCESSION:AR205452
C 147	8	40.0	11	1	AX628761	ACCESSION:AX628761	C 219	7.4	37.0	10	1	AR261814	ACCESSION:AR261814
C 148	8	40.0	11	1	AX629639	ACCESSION:AX629639	C 220	7.4	37.0	10	1	AR351673	ACCESSION:AR351673
C 149	8	40.0	11	1	AX629743	ACCESSION:AX629743	C 221	7.4	37.0	10	1	AR351674	ACCESSION:AR351674
C 150	8	40.0	11	1	AX630495	ACCESSION:AX630495	222	7.4	37.0	10	1	AX152442	ACCESSION:AX152442
C 151	8	40.0	11	1	AX632115	ACCESSION:AX632115	223	7.4	37.0	10	1	AX152741	ACCESSION:AX152741
C 152	8	40.0	11	1	AX632335	ACCESSION:AX632335	224	7.4	37.0	10	1	AX152778	ACCESSION:AX152778
C 153	8	40.0	11	1	AX632479	ACCESSION:AX632479	225	7.4	37.0	10	1	AX153207	ACCESSION:AX153207
C 154	8	40.0	11	1	AX632794	ACCESSION:AX632794	226	7.4	37.0	10	1	AX153311	ACCESSION:AX153311
C 155	8	40.0	11	1	AX632796	ACCESSION:AX632796	227	7.4	37.0	10	1	AX153312	ACCESSION:AX153312
C 156	8	40.0	11	1	BD124481	ACCESSION:BD124481	228	7.4	37.0	10	1	AX153453	ACCESSION:AX153453
C 157	8	40.0	11	1	AR135803	ACCESSION:AR135803	C 229	7.4	37.0	10	1	AX302591	ACCESSION:AX302591
C 158	8	40.0	12	1	AR168866	ACCESSION:AR168866	C 230	7.4	37.0	10	1	AX469413	ACCESSION:AX469413
C 159	7.8	39.0	11	1	AX169866	ACCESSION:AX169866	C 231	7.4	37.0	10	1	AX667118	ACCESSION:AX667118
C 160	7.8	39.0	11	1	AX319383	ACCESSION:AX319383	C 232	7.4	37.0	10	1	AX667119	ACCESSION:AX667119
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C 162	7.8	39.0	11	1	AX471766	ACCESSION:AX471766	234	7.4	37.0	10	1	BD161395	ACCESSION:BD161395
C 163	7.8	39.0	11	1	AX623493	ACCESSION:AX623493	235	7.4	37.0	10	1	BD166561	ACCESSION:BD166561
C 164	7.8	39.0	11	1	AX623691	ACCESSION:AX623691	236	7.4	37.0	10	1	BD166788	ACCESSION:BD166788
C 165	7.8	39.0	11	1	AX624406	ACCESSION:AX624406	237	7.4	37.0	10	1	BD166869	ACCESSION:BD166869
C 166	7.8	39.0	11	1	AX624475	ACCESSION:AX624475	238	7.4	37.0	10	1	BD166960	ACCESSION:BD166960
C 167	7.8	39.0	11	1	AX626034	ACCESSION:AX626034	239	7.4	37.0	10	1	BD167006	ACCESSION:BD167006
C 168	7.8	39.0	11	1	AX626284	ACCESSION:AX626284	240	7.4	37.0	10	1	BD167029	ACCESSION:BD167029
C 169	7.8	39.0	11	1	AX627660	ACCESSION:AX627660	241	7.4	37.0	10	1	BD167055	ACCESSION:BD167055
C 170	7.8	39.0	11	1	AX627817	ACCESSION:AX627817	C 242	7.4	37.0	10	1	BD167237	ACCESSION:BD167237
C 171	7.8	39.0	11	1	AX630914	ACCESSION:AX630914	243	7.4	37.0	11	1	AR301508	ACCESSION:AR301508
C 172	7.8	39.0	11	1	AX631112	ACCESSION:AX631112	C 244	7.4	37.0	11	1	AR301596	ACCESSION:AR301596
C 173	7.8	39.0	11	1	AX631827	ACCESSION:AX631827	C 245	7.4	37.0	11	1	AX339216	ACCESSION:AX339216
C 174	7.8	39.0	11	1	AX631896	ACCESSION:AX631896	246	7.4	37.0	11	1	AX393079	ACCESSION:AX393079
C 175	7.8	39.0	11	1	AX632493	ACCESSION:AX632493	247	7.4	37.0	11	1	AX470499	ACCESSION:AX470499
C 176	7.8	39.0	11	1	AX632794	ACCESSION:AX632794	248	7.4	37.0	11	1	AX471362	ACCESSION:AX471362
C 177	7.8	39.0	12	1	A06190	ACCESSION:A06190	C 249	7.4	37.0	11	1	AX471759	ACCESSION:AX471759
C 178	7.8	39.0	12	1	A61480	ACCESSION:A61480	250	7.4	37.0	11	1	AX471838	ACCESSION:AX471838
C 179	7.8	39.0	12	1	A71519	ACCESSION:A71519	C 251	7.4	37.0	11	1	AX623182	ACCESSION:AX623182
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGCG 14
Db 18 TGGACTCGCTGCG 6

RESULT 4
AR074734/c
LOCUS AR074734 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 31 from patent US 5955276.
ACCESSION AR074734
VERSION AR074734.1 GI:10001487
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 31 21-SEP-1999;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 56.0%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACTCGCTGCGACGCA 19
Db 17 GACAAGCTGCTAGCA 2

RESULT 5
AX339221/c
LOCUS AX339221 11 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 15 from Patent WO0196602.
ACCESSION AX339221
VERSION AX339221.1 GI:18135482
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE
1 Yang,A.L. and Festing,M.
AUTHORS Methods and materials to determine the p53 status of a sample by
TITLE determining the binding of p53 to a vector
JOURNAL Patent: WO 0196602-A 15 20-DEC-2001;
MEDICAL RESEARCH COUNCIL (GB)
FEATURES
Location/Qualifiers
source
1..11
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match
Best Local Similarity 55.0%; Score 11; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTCGCTGCG 14
Db 11 GACTCGCTGCG 1

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RESULT 6
AX350138/c
LOCUS AX350138 12 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 661 from Patent WO0202606.
ACCESSION AX350138
VERSION AX350138.1 GI:18615816
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Ratti,G. and Grandi,G.
AUTHORS Immunisation against Chlamydia pneumoniae
TITLE Patent: WO 0202606-A 661 10-JAN-2002;
JOURNAL Chiron S.p.A. (IT)
FEATURES
Location/Qualifiers
source
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/notes="Primer tail"

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Query Match
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 9 GCTGGCAGCGAC 20
Db 12 GCTAGCAGCGAC 1

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RESULT 7
AR180569
LOCUS AR180569 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 637 from patent US 6333152.
ACCESSION AR180569
VERSION AR180569.1 GI:20222602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 637 25-DEC-2001;
FEATURES
Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGACTCGCTG 12
Db 2 ATGGACTCTCTG 13

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RESULT 8
AR328418/c
LOCUS AR328418 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5820 from patent US 6566127.
ACCESSION AR328418
VERSION AR328418.1 GI:33714226
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions

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related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5820 20-MAY-2003;
Location/Qualifiers
1. .16
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Query Match
Best Local Similarity 52.0%; Score 10.4; DB 1; Length 16;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
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Db 16 GTACTCGCTGGC 5

RESULT 9
AX268358/c
LOCUS
DEFINITION
Sequence 7 from Patent WO0175127.
ACCESSION
AX268358
VERSION
AX268358.1 GI:16541576
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Nehls M. and Wattler S.
TITLE
Cloning system used in the construction of homologous recombination
vectors
JOURNAL
Patent: WO 0175127-A 7 11-OCT-2001;
Ingenium Pharmaceuticals AG (DE)
LOCATION/Qualifiers
1. .16
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz: Restriktionschnittstelle Sfi B"

Query Match
Best Local Similarity 52.0%; Score 10.4; DB 1; Length 16;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGC 14
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Db 16 GGCCTCGCTGGC 5

RESULT 10
AR125055/c
LOCUS
DEFINITION
Sequence 2 from patent US 6172281.
ACCESSION
AR125055
VERSION
AR125055.1 GI:14110449
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Van Mellaert, H., Botterman, J., Van Rie, J. and Joos, H.
TITLE
Recombinant plant expressing non-competitively binding BT
insecticidal crystal proteins
JOURNAL
Patent: US 6172281-A 2 09-JAN-2001;
LOCATION/Qualifiers
1. .15
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Query Match
Best Local Similarity 51.0%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 15
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Db 1 TGGAGCCGCTGACAC 15

RESULT 11
AR285771
LOCUS
DEFINITION
Sequence 143 from patent US 6528640.
ACCESSION
AR285771
VERSION
AR285771.1 GI:29723365
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A.,
Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE
Synthetic ribonucleic acids with RNase activity
JOURNAL
Patent: US 6528640-A 143 04-MAR-2003;
LOCATION/Qualifiers
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/mol_type="unassigned RNA"

Query Match
Best Local Similarity 51.0%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 16
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Db 1 TGGAGCCGCTGACAC 15

RESULT 12
AR397762
LOCUS
DEFINITION
Sequence 143 from patent US 6617438.
ACCESSION
AR397762
VERSION
AR397762.1 GI:40135008
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A.,
Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE
Oligoribonucleotides with enzymatic activity
JOURNAL
Patent: US 6617438-A 143 09-SEP-2003;
LOCATION/Qualifiers
1. .15
/organism="unknown"
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Query Match
Best Local Similarity 51.0%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCGCTGGCAC 16
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Db 1 TGGAGCCGCTGACAC 15

RESULT 13
AX624655
LOCUS
DEFINITION
Sequence 1696 from Patent WO02053774.
ACCESSION
AX624655
VERSION
AX624655.1 GI:28452596
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1696 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
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Db 2 TGGCAGGCAC 11

RESULT 14

AX632076 11 bp DNA linear PAT 21-FEB-2003
LOCUS
DEFINITION Sequence 9118 from Patent WO02053774.
ACCESSION AX632076
VERSION AX632076.1 GI:28467691

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9118 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

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Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
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Db 2 TGGCAGGCAC 11

RESULT 15

BD005894 15 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Novel probes for the detection of Mycobacteria.

ACCESSION BD005894
VERSION BD005894.1 GI:18634265
KEYWORDS JP 2001501825-A/105.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 15)
AUTHORS Stender,H., Lund,K. and Mollerup,T.A.
TITLE Novel probes for the detection of Mycobacteria
JOURNAL Patent: JP 2001501825-A 105 13-FEB-2001;
DAKO AS

COMMENT
OS Unidentified
PN JP 2001501825-A/105
PD 13-FEB-2001
PF 03-OCT-1997 JP 1998517095
PR 04-OCT-1996 DK 1096/96,18-OCT-1996 DK 1156/96 PR
05-MAY-1997 DK 0512/97

PI HENRIK STENDER,KARE LUND,TINA ANDRESEN MOLLERUP PC
C12P1/68,C07K14/00

CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
FT /organism="Unidentified".

FEATURES

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Query Match 50.0%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 17
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Db 5 CGCTGGCAGC 14

RESULT 16

AR175758 15 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 3 from patent US 6309859.
ACCESSION AR175758
VERSION AR175758.1 GI:17917057

KEYWORDS Unknown.
SOURCE
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Nishimura,O., Suenaga,M., Ohmae,H. and Tsuji,S.
TITLE Method for removing N-terminal methionine
JOURNAL Patent: US 6309859-A 3 30-OCT-2001;
Location/Qualifiers

FEATURES

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/mol_type="unassigned DNA"

Query Match 49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCCTGGCAGCA 19
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Db 3 TCCTGGCAGCA 15

RESULT 17

E13070 15 bp DNA linear PAT 27-APR-1998
LOCUS
DEFINITION Adaptor for constructing NT-3 expression vector.

ACCESSION E13070
VERSION E13070.1 GI:3251882
KEYWORDS JP 1997121886-A/3.
SOURCE unidentified

ORGANISM unidentified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Suenaga,M., Ohmae,H. and Nishimura,T.
TITLE PRODUCTION OF NEUROTROPHIN-3 COMPOUNDS
JOURNAL Patent: JP 1997121886-A 3 13-MAY-1997;
TAKEDA CHEM IND LTD

COMMENT
OS None
OC Artificial sequences.
PN JP 1997121886-A/3
PD 13-MAY-1997
PF 22-AUG-1996 JP 1996220963
PR 25-AUG-1995 JP 95P 217032
PI SUENAGA MASATO, OMAE HIROAKI, NISHIMURA TADASHI PC
C12P21/02,C07K14/48,C12N15/09/C12N1/21,C12P1/19), PC

(C12N1:19);
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 FH Key Location/Qualifiers
 FT source 1.15
 FT /organism='Artificial sequences'.
 FT Location/Qualifiers
 FT 1.15
 FT /organism='unidentified'
 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:32644'

FEATURES

source

Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 48;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGGCAGCA 19
 |||||
 Db 3 TCCCTGGCATGCA 15

RESULT 18
 E14044
 LOCUS E14044 15 bp DNA linear PAT 28-JUL-1999
 DEFINITION Adaptor DNA.
 ACCESSION E14044
 VERSION E14044.1 GI:5708727
 KEYWORDS JP 1997262093-A/3.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1. (bases 1 to 15)
 AUTHORS Omae, H., Suenaga, M. and Nishimura, T.
 TITLE ACTIVATION OF PROTEIN
 JOURNAL Patent: JP 1997262093-A 3 07-OCT-1997;
 COMMENT TAKEDA CHEM IND LTD
 OS None
 OC Artificial sequences.
 PN JP 1997262093-A/3
 PD 07-OCT-1997
 PF 28-MAR-1996 JP 1996074775
 PI OMAE HIROAKI, SUENAGA MASATO, NISHIMURA TADASHI PC
 C12P21/00, C07H21/04, C12N1/21, C12N15/09, C12P21/02, A61K38/22, PC
 A61K38/22,
 PC C07K14/48, (C12N1:19), (C12P21/02, C12R1:19); CC
 strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FT source 1.15
 FT /organism='Artificial sequences'.
 FT Location/Qualifiers
 FT 1.15
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 FT /mol_type='genomic DNA'
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Query Match 49.0%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 48;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGGCAGCA 19
 |||||
 Db 3 TCCCTGGCATGCA 15

RESULT 19
 E15462
 LOCUS E15462 15 bp RNA linear PAT 28-JUL-1999
 DEFINITION Adaptor.

ACCESSION E15462
 VERSION E15462.1 GI:5710145
 KEYWORDS JP 1998072489-A/3.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 15)
 Nishimura, T., Suenaga, M., Omae, H. and Tsuji, S.
 TITLE REMOVAL OF N-TERMINAL METHIONINE
 JOURNAL Patent: JP 1998072489-A 3 17-MAR-1998;
 COMMENT TAKEDA CHEM IND LTD

OS None

OC Artificial sequences.

PN JP 1998072489-A/3

PD 17-MAR-1998

PF 13-JUN-1997 JP 1997156777

PI 14-JUN-1996 JP 96P 154634

PC NISHIMURA TADASHI, SUENAGA MASATO, OMAE HIROAKI, TSUJI SHINJI

C07K12/12, C12N15/09, C12P21/02, C12P21/02, C12P21/02, C12R1:19;

CC strandedness: Single;

CC topology: Linear;

CC hypothetical: No;

FH Key Location/Qualifiers

FT source 1.15

FT /organism='Artificial sequences'.

FT Location/Qualifiers

FT 1.15

FT /organism='unidentified'

FT /mol_type='genomic RNA'

FT /db_xref='taxon:32644'

FEATURES

source

Query Match 49.0%; Score 9.8; DB 1; Length 15;
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 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGGCAGCA 19
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 Db 3 TCCCTGGCATGCA 15

RESULT 20
 AR193001

LOCUS

DEFINITION

Sequence 8489 from patent US 6346398.

AR193001

ACCESSION

AR193001.1

VERSION

GI:20238966

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 15)

AUTHORS

Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

TITLE

Method and reagent for the treatment of diseases or conditions

JOURNAL

related to levels of vascular endothelial growth factor receptor

Patent: US 6346398-A 8489 12-FEB-2002;

FEATURES

Location/Qualifiers

source

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/mol_type='unassigned DNA'

Query Match

49.0%; Score 9.8; DB 1; Length 15;

Best Local Similarity

84.6%; Pred. No. 48;

Matches 11; Conservative

0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGG 13

|||||

Db 1 ATGGAATCTCTGG 13

|||||

RESULT 21

AR326741

LOCUS

AR326741 15 bp RNA linear PAT 17-AUG-2003

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DEFINITION Sequence 4143 from patent US 6566127.
ACCESSION AR326741
VERSION AR326741.1 GI:33712549
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 15)
  Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  Patent: US 6566127-A 4143 20-MAY-2003;
JOURNAL
  Location/Qualifiers
FEATURES
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    /mol_type="unassigned RNA"

Query Match          49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGG 13
    |||||
DB 1 ATGGAATCTCTGG 13

RESULT 22
AX698541
LOCUS AX698541 15 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 30 from Patent WO03010335.
ACCESSION AX698541
VERSION AX698541.1 GI:29499369
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
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  Mirel,D.B., Erlich,H.A., Bugawan,T.L., Noble,J.A. and Valdez,A.M.
  TITLE
  IL-4 receptor sequence variation associated with type 1 diabetes
  JOURNAL
  Patent: WO 03010335-A 30 06-FEB-2003;
  Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="primer"

Query Match          49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTGGCA 15
    |||||
DB 3 GGCTCCCTGGCA 15

RESULT 23
BD141542
LOCUS BD141542 15 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for production of recombinant protein.
ACCESSION BD141542
VERSION BD141542.1 GI:23236487
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1 (bases 1 to 15)
  Ito,T., Tanaka,Y. and Kondo,M.
  TITLE
  Method for production of recombinant protein
  JOURNAL
  Patent: WO 0208417-A 70 31-JAN-2002;
  TAKEDA CHEMICAL INDUSTRIES LTD,TAKASHI ITO,YOKO TANAKA, MITSUYO
  KONDO
Sequence 4143 from patent US 6566127.
ACCESSION AR326741
VERSION AR326741.1 GI:33712549
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 15)
  Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  Patent: US 6566127-A 4143 20-MAY-2003;
JOURNAL
  Location/Qualifiers
FEATURES
  source
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    /mol_type="unassigned RNA"

Query Match          49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGACTCGCTGG 13
    |||||
DB 1 ATGGAATCTCTGG 13

RESULT 24
BD176038
LOCUS BD176038 15 bp DNA linear PAT 18-MAR-2003
DEFINITION Method for production of recombinant protein.
ACCESSION BD176038
VERSION BD176038.1 GI:29121742
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1 (bases 1 to 15)
  Ito,T., Tanaka,Y. and Kondo,M.
  TITLE
  Method for production of recombinant protein
  JOURNAL
  Patent: JP 2002272481-A 70 24-SEP-2002;
  TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT
  OS Artificial Sequence
  PN JP 2002272481-A/70
  PD 24-SEP-2002
  PF 25-JUL-2001 JP 2001224117
  PI TAKASHI ITO,YOKO TANAKA,MITSUYO KONDO
  PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,PC
  A61K38/00,
  PC A61P43/00,C12P21/02,C12R1.01,C12N15/00,C12N5/00,A61K37/02 CC
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  FH Key
  FT source
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Query Match          49.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TCGCTGCACGCA 19
    |||||
DB 3 TCGCTTCCACGCA 15

RESULT 25
AX624728/c
LOCUS AX624728 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1769 from Patent WO02053774.
ACCESSION AX624728

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VERSION AX624728.1 GI:28452669
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Petersohn, D., Conradt, M. and Hofmann, K.
JOURNAL Method for determining homeostasis of the skin
PATENT: WO 02053774-A 1769 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGGCAC 20
| | | | | | | | | |
Db 11 CAGGCAGGCAC 1

RESULT 26
AX632149/c
LOCUS Homo sapiens
DEFINITION Sequence 9191 from Patent WO02053774.
ACCESSION AX632149
VERSION AX632149.1 GI:28467764
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Petersohn, D., Conradt, M. and Hofmann, K.
JOURNAL Method for determining homeostasis of the skin
PATENT: WO 02053774-A 9191 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGGCAC 20
| | | | | | | | | |
Db 11 CAGGCAGGCAC 1

RESULT 27
AX71521/c
LOCUS Homo sapiens
DEFINITION Sequence 80 from Patent WO9813521.
ACCESSION AX71521
VERSION AX71521.1 GI:4775133
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Petersohn, D., Conradt, M. and Hofmann, K.
JOURNAL Method for determining homeostasis of the skin
PATENT: WO 02053774-A 80 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES Location/Qualifiers
source 1. .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 47.0%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGG 13
| | | | | | | | | |
Db 11 GGACTCGTGG 1

RESULT 28
AR349598
LOCUS Homo sapiens
DEFINITION Sequence 34 from patent US 6586180.
ACCESSION AR349598
VERSION AR349598.1 GI:33750396
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Ruffner, D.E., Pierce, M.L. and Chen, Z.
AUTHORS Directed antisense libraries
TITLE Patent: US 6586180-A 34 01-JUL-2003;
JOURNAL Location/Qualifiers
FEATURES Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTGG 13
| | | | | | | | | |
Db 3 GGATTCGCTGG 13

RESULT 29
BD225400
LOCUS Targeting antisense library.
DEFINITION Targeting antisense library.
ACCESSION BD225400
VERSION BD225400.1 GI:33035170
KEYWORDS JP 2002509733-A/34.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Ruffner, D.E., Pierce, M.L. and Chen, Z.
TITLE Targeting antisense library
JOURNAL Patent: JP 2002509733-A 34 02-APR-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT OS Herpes simplex virus
PN JP 2002509733-A/34
PD 02-APR-2002
PF 28-MAR-1998 JP 2000541344
PR 28-MAR-1998 US 60/079792, 06-NOV-1998 US 60/107504 PT
DUANE E RUFFNER, MICHAEL L PIERCE, ZHIDONG CHEN PQ
C12N15/09, C12Q1/68//A61K48/00, C12N15/00
CC Targeting antisense library
FH Key Location/Qualifiers
FT source 1. .14
/organism="Herpes simplex virus".

FEATURES Location/Qualifiers
source 1. .14
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/db_xref="taxon:32644"
Query Match      47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGACTCGTGG 13
Db      3 GGATTCGTGG 13

RESULT 30
BD239415
LOCUS      BD239415
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239415
VERSION    BD239415.1 GI:33049185
KEYWORDS   JP 2002534056-A/833.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLES      Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 833 15-OCT-2002;
            GENZYME CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2002534056-A/833
            PD 15-OCT-2002
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
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            /db_xref="taxon:32644"

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Query Match      45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCACGCGAC 20
Db      9 GGCACGCGAC 1

RESULT 32
AX153274
LOCUS      AX153274
DEFINITION Sequence 1189 from Patent WO0138577.
ACCESSION AX153274
VERSION    AX153274.1 GI:14534925
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLES      Human transcriptomes
JOURNAL     Patent: WO 0138577-A 1189 31-MAY-2001;

/db_xref="taxon:32644"
Query Match      47.0%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGACTCGTGG 13
Db      3 GGATTCGTGG 13

RESULT 30
BD239415
LOCUS      BD239415
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239415
VERSION    BD239415.1 GI:33049185
KEYWORDS   JP 2002534056-A/833.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLES      Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 833 15-OCT-2002;
            GENZYME CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2002534056-A/833
            PD 15-OCT-2002
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
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            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            /organism='Homo sapiens (human)'
            /db_xref="taxon:32644"

FEATURES
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            /db_xref="taxon:32644"

Query Match      45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCAGCGCA 19
Db      2 TGGCAGCGCA 10

RESULT 31
BD239954/c

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FEATURES
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          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 45.0%; Score 9; DB 1; Length 10;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 33
LOCUS AX624613 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1654 from Patent WO02053774.
ACCESSION AX624613
VERSION AX624613.1 GI:28452554
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL Patent: WO 02053774-A 1654 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
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          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 45.0%; Score 9; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 3 GGCACGCAC 11

RESULT 34
LOCUS AX625787 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2828 from Patent WO02053774.
ACCESSION AX625787
VERSION AX625787.1 GI:28453728
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL Patent: WO 02053774-A 2828 11-JUL-2002;
  FEATURES
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      Location/Qualifiers
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          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 45.0%; Score 9; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 35
LOCUS AX632034 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9076 from Patent WO02053774.
ACCESSION AX632034
VERSION AX632034.1 GI:28467649
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL Patent: WO 02053774-A 9076 11-JUL-2002;
  FEATURES
    source
      Location/Qualifiers
        1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 45.0%; Score 9; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 3 GGCACGCAC 11

RESULT 36
LOCUS AR135801 12 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 3 from patent US 6136568.
ACCESSION AR135801
VERSION AR135801.1 GI:14476473
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 12)
  AUTHORS Hiatt,A.C. and Rose,F.D.
  TITLE De novo polynucleotide synthesis using rolling templates
  JOURNAL Patent: US 6136568-A 3 24-OCT-2000;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 45.0%; Score 9; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
Db 3 ATGGACTCG 11

RESULT 37
LOCUS AR135802 12 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 4 from patent US 6136568.
ACCESSION AR135802
VERSION AR135802.1 GI:14476474
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

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REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	Query Match	Best Local Similarity	Mismatches	Indels	Gaps	Length	DB	Patent	Year
Unclassified.	1 (bases 1 to 12)	Hiatt, A.C. and Rose, F.D.	De novo polynucleotide synthesis using rolling templates	Patent: US 6136568-A 4 24-OCT-2000;	Location/Qualifiers	1. .12	/organism="unknown"	/mol_type="unassigned DNA"						
Query Match	45.0%; Score 9; DB 1;	Length 12;												
Best Local Similarity	100.0%; Pred. No. 57;													
Mismatches	9; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;										
QY	1 ATGGACTCG 9													
Db	4 ATGGACTCG 12													
RESULT 38	AR094449/c													
LOCUS	AR094449	Sequence 44 from patent US 6001648.												
DEFINITION	AR094449													
ACCESSION	AR094449													
VERSION	AR094449.1	GI:100211381												
KEYWORDS														
SOURCE	Unknown.													
ORGANISM	Unknown.													
REFERENCE	1 (bases 1 to 13)	McCall, M.J., Hendry, P. and Lockett, T.	Optimized minizymes and miniribozymes and uses thereof	Patent: US 6001648-A 44 14-DEC-1999;	Location/Qualifiers	1. .13	/organism="unknown"	/mol_type="unassigned DNA"						
Query Match	45.0%; Score 9; DB 1;	Length 13;												
Best Local Similarity	100.0%; Pred. No. 63;													
Mismatches	9; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;										
QY	2 TGGACTCGC 10													
Db	9 TGGACTCGC 1													
RESULT 39	AR154534/c													
LOCUS	AR154534	Sequence 14 from patent US 6238917.												
DEFINITION	AR154534													
ACCESSION	AR154534													
VERSION	AR154534.1	GI:15122587												
KEYWORDS														
SOURCE	Unknown.													
ORGANISM	Unknown.													
REFERENCE	1 (bases 1 to 13)	Hendry, P. and McCall, M.J.	Asymmetric hammerhead ribozymes	Patent: US 6238917-A 14 29-MAY-2001;	Location/Qualifiers	1. .13	/organism="unknown"	/mol_type="unassigned DNA"						
Query Match	45.0%; Score 9; DB 1;	Length 13;												
Best Local Similarity	100.0%; Pred. No. 63;													
Mismatches	9; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;										
QY	2 TGGACTCGC 10													
Db	9 TGGACTCGC 1													
RESULT 40	AR175358/c													
LOCUS	AR175358	Sequence 81 from patent US 6309823.												
DEFINITION	AR175358													
ACCESSION	AR175358													
VERSION	AR175358.1	GI:17916657												

AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 30 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 43
AR362041/c
LOCUS AR362041 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 34 from patent US 6600026.
ACCESSION AR362041
VERSION AR362041.1 GI:33770192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 34 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 44
AR362043/c
LOCUS AR362043 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 36 from patent US 6600026.
ACCESSION AR362043
VERSION AR362043.1 GI:33770194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 36 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 45
AR362049/c
LOCUS AR362049 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 42 from patent US 6600026.
ACCESSION AR362049
VERSION AR362049.1 GI:33770200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 42 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 46
AR362051/c
LOCUS AR362051 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 44 from patent US 6600026.
ACCESSION AR362051
VERSION AR362051.1 GI:33770202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 44 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 47
AX078151/c
LOCUS AX078151 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 45 from Patent WO0106016.
ACCESSION AX078151
VERSION AX078151.1 GI:13157896
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS

Db 10 ATGGACTCG 2
RESULT 45
AR362049/c
LOCUS AR362049 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 42 from patent US 6600026.
ACCESSION AR362049
VERSION AR362049.1 GI:33770200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 42 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 46
AR362051/c
LOCUS AR362051 13 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 44 from patent US 6600026.
ACCESSION AR362051
VERSION AR362051.1 GI:33770202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yu.C.
TITLE Electronic methods for the detection of analytes utilizing monolayers
JOURNAL Patent: US 6600026-A 44 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 47
AX078151/c
LOCUS AX078151 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 45 from Patent WO0106016.
ACCESSION AX078151
VERSION AX078151.1 GI:13157896
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS

TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 45 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES Location/Qualifiers
source
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic."

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
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Db 10 ATGGACTCG 2

RESULT 48
AX078153/c
LOCUS AX078153 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 47 from Patent WO0106016.
ACCESSION AX078153
VERSION AX078153.1 GI:13157898
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 47 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES Location/Qualifiers
source
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic."

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
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Db 10 ATGGACTCG 2

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 49
AX078157/c
LOCUS AX078157 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 51 from Patent WO0106016.
ACCESSION AX078157
VERSION AX078157.1 GI:13157902
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 51 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES Location/Qualifiers
source
1. .13
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/db_xref="taxon:32630"
/note="synthetic."

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

Query Match 45.0%; Score 9; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 50
AX078159/c
LOCUS AX078159 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 53 from Patent WO0106016.
ACCESSION AX078159
VERSION AX078159.1 GI:13157904
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 53 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES Location/Qualifiers
source
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic."

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
|||||
Db 10 ATGGACTCG 2

RESULT 51
AX078165/c
LOCUS AX078165 13 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 59 from Patent WO0106016.
ACCESSION AX078165
VERSION AX078165.1 GI:13157910
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 59 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES Location/Qualifiers
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1. .13
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic."

Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
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Db 10 ATGGACTCG 2

RESULT 52
AX078167/c
LOCUS AX078167 13 bp DNA linear PAT 22-FEB-2001

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DEFINITION Sequence 61 from Patent WO0106016.
ACCESSION AX078167
VERSION AX078167.1 GI:13157912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bandad,C. and Yu,C.
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 61 25-JAN-2001;
Clinical Micro Sensors, Inc. (US)
FEATURES
source
1. .13
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic."
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 53
BD209805/c
LOCUS 13 bp DNA linear PAT 17-JUL-2003
DEFINITION Electronic detection of nucleic acids using monolayers.
ACCESSION BD209805
VERSION BD209805.1 GI:33019575
KEYWORDS JP 2002513592-A/45.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS BAMDAD,C. and YU,C.
TITLE Electronic detection of nucleic acids using monolayers
JOURNAL Patent: JP 2002513592-A 45 14-MAY-2002;
CLINICAL MICRO SENSORS INC
OS Artificial Sequence
PN JP 2002513592-A/45
PD 14-MAY-2002
PF 27-JAN-1999 JP 2000547270
PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR
17-AUG-1998 US 09/135183
PI CYNTHIA BAMDAD,CHANGYUN YU
PC C12Q1/68,C07F17/00,C07F19/00,C12N15/09,C12P19/34,G01N27/327,
G01N27/416,
PC G01N33/53,C12N15/00,G01N27/30,G01N27/46
CC Description of Artificial Sequence: synthetic FH Key
FT source 1. .13
FT /organism='Artificial Sequence'.
FEATURES
source
1. .13
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 54
BD209811/c
LOCUS 13 bp DNA linear PAT 17-JUL-2003
DEFINITION Electronic detection of nucleic acids using monolayers.
ACCESSION BD209811
VERSION BD209811.1 GI:33019581
KEYWORDS JP 2002513592-A/51.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS BAMDAD,C. and YU,C.
TITLE Electronic detection of nucleic acids using monolayers
JOURNAL Patent: JP 2002513592-A 51 14-MAY-2002;
CLINICAL MICRO SENSORS INC
OS Artificial Sequence
PN JP 2002513592-A/51
PD 14-MAY-2002
PF 27-JAN-1999 JP 2000547270
PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR
17-AUG-1998 US 09/135183
PI CYNTHIA BAMDAD,CHANGYUN YU
PC C12Q1/68,C07F17/00,C07F19/00,C12N15/09,C12P19/34,G01N27/327,
G01N27/416,
PC G01N33/53,C12N15/00,G01N27/30,G01N27/46
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source
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Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTCG 9
Db 10 ATGGACTCG 2
RESULT 54
BD209811/c
LOCUS 13 bp DNA linear PAT 17-JUL-2003
DEFINITION Electronic detection of nucleic acids using monolayers.
ACCESSION BD209811
VERSION BD209811.1 GI:33019581
KEYWORDS JP 2002513592-A/51.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS BAMDAD,C. and YU,C.
TITLE Electronic detection of nucleic acids using monolayers
JOURNAL Patent: JP 2002513592-A 51 14-MAY-2002;
CLINICAL MICRO SENSORS INC
OS Artificial Sequence
PN JP 2002513592-A/51
PD 14-MAY-2002
PF 27-JAN-1999 JP 2000547270
PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR
17-AUG-1998 US 09/135183
PI CYNTHIA BAMDAD,CHANGYUN YU
PC C12Q1/68,C07F17/00,C07F19/00,C12N15/09,C12P19/34,G01N27/327,
G01N27/416,
PC G01N33/53,C12N15/00,G01N27/30,G01N27/46
CC Description of Artificial Sequence: synthetic FH Key
FT source 1. .13
FT /organism='Artificial Sequence'.
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1. .13
Location/Qualifiers
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/db_xref="taxon:32630"

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OS	Artificial Sequence	JP 2002513592-A/59	JP 2000547270	60/084425, 06-MAY-1998 US	60/084509 PR
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PD	14-MAY-2002				
PF	27-JAN-1999	JP 2000547270			
PR	06-MAY-1998 US	60/084425, 06-MAY-1998 US			
PI	17-AUG-1998 US	09/135183			
PI	CYNTHIA BAMDAD, CHANGYUN YU				
PC	C12Q1/68, C07F17/00, C07F19/00, C12N15/09, C12P19/34, G01N27/327, G01N27/416,				
PC	G01N33/53, C12N15/00, G01N27/30, G01N27/46				
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Location/Qualifiers					
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FT	1. .13				
FT	Location/Qualifiers	/organism="synthetic construct"			
FT	/mol_type="genomic DNA"				
FT	/db_xref="taxon:32630"				
Query Match		45.0%; Score 9; DB 1; Length 13;			
Best Local Similarity		100.0%; Pred. No. 63;			
Matches	9; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1 ATGGACTCG 9				
Db	10 ATGGACTCG 2				
RESULT 58					
BD209821/c					
LOCUS		13 bp DNA linear	PAT 17-JUL-2003		
DEFINITION		Electronic detection of nucleic acids using monolayers.			
ACCESSION		BD209821			
VERSION		BD209821.1 GI:33019591			
KEYWORDS		JP 2002513592-A/61.			
SOURCE		synthetic construct			
ORGANISM		artificial sequences.			
REFERENCE		1 (bases 1 to 13)			
AUTHORS		Bamdad, C. and Yu, C.			
TITLE		Electronic detection of nucleic acids using monolayers			
JOURNAL		Patent: JP 2002513592-A 61 14-MAY-2002;			
COMMENT		CLINICAL MICRO SENSORS INC			
OS	Artificial Sequence				
PN	JP 2002513592-A/61				
PD	14-MAY-2002				
PF	27-JAN-1999	JP 2000547270			
PR	06-MAY-1998 US	60/084425, 06-MAY-1998 US			
PI	17-AUG-1998 US	09/135183			
PI	CYNTHIA BAMDAD, CHANGYUN YU				
PC	C12Q1/68, C07F17/00, C07F19/00, C12N15/09, C12P19/34, G01N27/327, G01N27/416,				
PC	G01N33/53, C12N15/00, G01N27/30, G01N27/46				
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Location/Qualifiers					
FT	source	1. .13			
FT	Location/Qualifiers	/organism='Artificial Sequence'.			
FT	1. .13				
FT	Location/Qualifiers	/organism="synthetic construct"			
FT	/mol_type="genomic DNA"				
FT	/db_xref="taxon:32630"				
Query Match		45.0%; Score 9; DB 1; Length 13;			
Best Local Similarity		100.0%; Pred. No. 63;			
Matches	9; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1 ATGGACTCG 9				
Db	10 ATGGACTCG 2				

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RESULT 59
AR034976
LOCUS AR034976 18 from patent US 5971697. 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5971697.
ACCESSION AR034976
VERSION AR034976.1 GI:5951644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 5971697-A 18 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..12
/mol_type="unassigned DNA"
Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12
RESULT 60
AR034978
LOCUS AR034978 20 from patent US 5971697. 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5971697.
ACCESSION AR034978
VERSION AR034978.1 GI:5951646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 5971697-A 20 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..12
/mol_type="unassigned DNA"
Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12
RESULT 61
AR082060
LOCUS AR082060 18 from patent US 5972693. 12 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 18 from patent US 5972693.
ACCESSION AR082060
VERSION AR082060.1 GI:10008786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Apparatus for identifying, classifying, or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 5972693-A 18 26-OCT-1999;
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Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12
RESULT 62
AR082062
LOCUS AR082062 20 from patent US 5972693. 12 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 20 from patent US 5972693.
ACCESSION AR082062
VERSION AR082062.1 GI:10008788
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Apparatus for identifying, classifying, or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 5972693-A 20 26-OCT-1999;
FEATURES
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Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGC 12
RESULT 63
AR118451
LOCUS AR118451 18 from patent US 6141657. 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6141657.
ACCESSION AR118451
VERSION AR118451.1 GI:14099357
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying classifying or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 6141657-A 18 31-OCT-2000;
FEATURES
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Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGC 12
RESULT 64
AR118451
LOCUS AR118451 18 from patent US 6141657. 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6141657.
ACCESSION AR118451
VERSION AR118451.1 GI:14099357
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying classifying or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 6141657-A 18 31-OCT-2000;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACTCGCTGGCAC 16
Db 1 AGTCGCTGGTAC 12
RESULT 64
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AR118453
LOCUS AR118453 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6141657.
ACCESSION AR118453
VERSION AR118453.1 GI:14099359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying classifying or quantifying DNA
JOURNAL sequences in a sample without sequencing
PATENT: US 6141657-A 20 31-OCT-2000;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
| | | | |
Db 1 AGTCGCTGGGC 12

RESULT 65
AR151019
LOCUS AR151019 12 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 18 from patent US 6231812.
ACCESSION AR151019
VERSION AR151019.1 GI:15117069
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for indentifying, classifying, or quantifying
JOURNAL protein sequences in a sample without sequencing
PATENT: US 6231812-A 18 15-MAY-2001;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
| | | | |
Db 1 AGTCGCTGGGC 12

RESULT 66
AR151021
LOCUS AR151021 12 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 20 from patent US 6231812.
ACCESSION AR151021
VERSION AR151021.1 GI:15117071
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for indentifying, classifying, or quantifying
JOURNAL protein sequences in a sample without sequencing
PATENT: US 6231812-A 20 15-MAY-2001;
FEATURES
Location/Qualifiers
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source
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/mol_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
| | | | |
Db 1 AGTCGCTGGGC 12

RESULT 67
AR199166
LOCUS AR199166 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6355423.
ACCESSION AR199166
VERSION AR199166.1 GI:20249240
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 22 12-MAR-2002;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
| | | | |
Db 1 AGTCGCTGGTAC 12

RESULT 68
AR199168
LOCUS AR199168 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 6355423.
ACCESSION AR199168
VERSION AR199168.1 GI:20249242
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 24 12-MAR-2002;
FEATURES
Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGTAC 12

RESULT 69
AR218175
LOCUS AR218175 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 18 from patent US 6418382.
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AR218175
ACCESSION AR218175.1 GI:23318621
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 6418382-A 18 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGTAC 12

RESULT 70
LOCUS AR218177 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 20 from patent US 6418382.
ACCESSION AR218177
VERSION AR218177.1 GI:23318623
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 6418382-A 20 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGTAC 12

RESULT 71
LOCUS AR222615 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 18 from patent US 6432361.
ACCESSION AR222615
VERSION AR222615.1 GI:23330246
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6432361-A 18 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGGCG 12

RESULT 72
LOCUS AR222617 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6432361.
ACCESSION AR222617
VERSION AR222617.1 GI:23330248
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6432361-A 20 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGTAC 12

RESULT 73
LOCUS AR231653 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 18 from patent US 6453245.
ACCESSION AR231653
VERSION AR231653.1 GI:27272810
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6453245-A 18 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGGCG 12

RESULT 74
LOCUS AR231655 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 20 from patent US 6453245.
ACCESSION AR231655

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
| | | | | | | | | | | |
Db 1 AGTCGCTGGTAC 12

RESULT 72
LOCUS AR222617 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6432361.
ACCESSION AR222617
VERSION AR222617.1 GI:23330248
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6432361-A 20 13-AUG-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
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Db 1 AGTCGCTGGGCG 12

RESULT 73
LOCUS AR231653 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 18 from patent US 6453245.
ACCESSION AR231653
VERSION AR231653.1 GI:27272810
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6453245-A 18 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCAC 16
| | | | | | | | | | | |
Db 1 AGTCGCTGGGCG 12

RESULT 74
LOCUS AR231655 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 20 from patent US 6453245.
ACCESSION AR231655

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VERSION      AR231655.1  GI:27272812
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Rothberg, J.M., Deem, M.W. and Simpson, J.W.
TITLE        Method and apparatus for identifying, classifying, or quantifying
              protein sequences in a sample without sequencing
JOURNAL      Patent: US 6453245-A 20 17-SEP-2002;
              Location/Qualifiers
FEATURES     source
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              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5  ACTCGCTGGCAC 16
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Db   1  ACTCGCTGGCGC 12

RESULT 75
LOCUS      BD238599
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238599
VERSION    BD238599.1  GI:33048369
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 10)
            Roberts, B.L. and Shankara, S.
            Preparation and use of superior vaccines
            TITLE
            JOURNAL
            GENZYME CORP
            Patent: JP 2002534056-A 17 15-OCT-2002;
            COMMENT
            OS Homo sapiens (human)
            PN JP 2002534056-A/17
            PD 15-OCT-2002
            PF 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS, SRINIVAS SHANKARA
            PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            GOIN37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
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VERSION      AR231655.1  GI:27272812
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Rothberg, J.M., Deem, M.W. and Simpson, J.W.
TITLE        Method and apparatus for identifying, classifying, or quantifying
              protein sequences in a sample without sequencing
JOURNAL      Patent: US 6453245-A 20 17-SEP-2002;
              Location/Qualifiers
FEATURES     source
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Query Match      44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5  ACTCGCTGGCAC 16
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Db   1  ACTCGCTGGCGC 12

RESULT 76
LOCUS      BD239966
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239966
VERSION    BD239966.1  GI:33049736
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 10)
            Roberts, B.L. and Shankara, S.
            Preparation and use of superior vaccines
            TITLE
            JOURNAL
            GENZYME CORP
            Patent: JP 2002534056-A 1384 15-OCT-2002;
            COMMENT
            OS Homo sapiens (human)
            PN JP 2002534056-A/1384
            PD 15-OCT-2002
            PF 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS, SRINIVAS SHANKARA
            PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            GOIN37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
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            /mol_type="genomic DNA"

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/db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4  GACTCGCTGC 13
    |||||
Db   1  GACCCGCTGC 10

RESULT 76
LOCUS      BD239966
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239966
VERSION    BD239966.1  GI:33049736
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 10)
            Roberts, B.L. and Shankara, S.
            Preparation and use of superior vaccines
            TITLE
            JOURNAL
            GENZYME CORP
            Patent: JP 2002534056-A 1384 15-OCT-2002;
            COMMENT
            OS Homo sapiens (human)
            PN JP 2002534056-A/1384
            PD 15-OCT-2002
            PF 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS, SRINIVAS SHANKARA
            PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            GOIN37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            /organism='Homo sapiens (human)'.
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9  GCTGGCAGCG 18
    |||||
Db   1  GCTGGCAGGC 10

RESULT 77
ES4650

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LOCUS      E54650
DEFINITION Human normal liver cell expression genes.
ACCESSION  E54650
VERSION    E54650.1 GI:22556133
KEYWORDS   JP 2001211883-A/2
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Fukuyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
            Human normal liver cell expression genes
            Patent: JP 2001211883-A 2 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2001211883-A/2
            PD 07-AUG-2001
            PF 31-JAN-2000 JP 2000023170
            PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
            YAMASHITA
            PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
            CC
            FH Key Location/Qualifiers.
FEATURES   source
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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
Db 1 TGGACGGCCT 10

RESULT 78
AX152491/c
LOCUS      AX152491
DEFINITION Sequence 406 from Patent WO0138577.
ACCESSION  AX152491
VERSION    AX152491.1 GI:14534142
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 406 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   source
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            /db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGACGGCAC 20
Db 10 TGGACGGAAC 1

RESULT 79
AX301297/c
LOCUS      AX301297
DEFINITION Sequence 11 from Patent WO0185941.

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ACCESSION  AX301297
VERSION    AX301297.1 GI:17382380
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 11 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGACGGCAC 20
Db 10 TGGACGGAAC 1

RESULT 80
BD166770
LOCUS      BD166770
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166770
VERSION    BD166770.1 GI:27872582
KEYWORDS   JP 2002209591-A/315.
SOURCE     unidentified
            unclassified.
ORGANISM   1 (bases 1 to 10)

REFERENCE
AUTHORS    Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 315 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/315
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
            YAMASHITA
            PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
            PC C12P21/08,
            PC C12N15/00
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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
Db 1 TGGACGGCCT 10

RESULT 81
BD166807
LOCUS      BD166807
DEFINITION Sequence 11 from Patent WO0185941.

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DEFINITION Human liver disease-expressing genes.
ACCESSION BD166807
VERSION BD166807.1 GI:27872619
KEYWORDS JP 2002209591-A/352.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 352 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/352
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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/db_xref='taxon:32644'

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
DB 1 TGGACCCGCT 10

RESULT 83
LOCUS BD167022 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167022
VERSION BD167022.1 GI:27872834
KEYWORDS JP 2002209591-A/567.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 567 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/567
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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source
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/db_xref='taxon:32644'

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTCGCT 11
DB 1 TGGACCCGCT 10

RESULT 84
LOCUS BD167056 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167056
VERSION BD167056.1 GI:27872868
KEYWORDS JP 2002209591-A/601.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 601 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/601
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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source
Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

DEFINITION Human liver disease-expressing genes.
ACCESSION BD166975
VERSION BD166975.1 GI:27872787
KEYWORDS JP 2002209591-A/520.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 520 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/520
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
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PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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source
Location/Qualifiers
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DEFINITION Human liver disease-expressing genes.
ACCESSION BD166975
VERSION BD166975.1 GI:27872787
KEYWORDS JP 2002209591-A/520.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 520 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/520
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
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PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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YAMASHITA
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CC Human liver disease-expressing genes
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       /organism="unidentified"
       /mol_type="genomic DNA"
       /db_xref="taxon:32644"

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGACTCGCT 11
   |||||
Db 1 TGGACGCGCT 10

RESULT 85
BD167184
LOCUS Human liver disease-expressing genes. linear PAT 17-JAN-2003
DEFINITION BD167184
ACCESSION BD167184.1 GI:27872996
VERSION JP 200209591-A/729.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1. (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 200209591-A 729 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 200209591-A/729
PD 30-JUL-2002
PI 19-JAN-2001 JP 2001012328
PF KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
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PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGACTCGCT 11
   |||||
Db 1 TGGACGCGCT 10

RESULT 86
AX470770
LOCUS Sequence 347 from Patent WO2053773. linear PAT 09-AUG-2002
DEFINITION AX470770
ACCESSION AX470770
VERSION AX470770.1 GI:22205895
KEYWORDS

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Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stresses or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 347 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGGCAC 20
   |||||
Db 2 TGGCGGCAC 11

RESULT 87
AX471056
LOCUS Sequence 633 from Patent WO2053773. linear PAT 09-AUG-2002
DEFINITION AX471056
ACCESSION AX471056
VERSION AX471056.1 GI:22206181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stresses or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 633 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCTGGCAGGC 18
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Db 1 GCTGGCAGGC 10

RESULT 88
AX471099/c
LOCUS Sequence 676 from Patent WO2053773. linear PAT 09-AUG-2002
DEFINITION AX471099
ACCESSION AX471099
VERSION AX471099.1 GI:22206224
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stresses or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 676 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
   source
       Location/Qualifiers
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Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGGC 14
Db 10 ACTGCTGGC 1

RESULT 89
AX471193
LOCUS AX471193 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 770 from Patent WO02053773.
ACCESSION AX471193
VERSION AX471193.1 GI:22206318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Hofmann, K., Conradt, M. and Petersohn, D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 770 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
Location/Qualifiers
1..11
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Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGACTCGCTG 12
Db 2 GGACTCACTG 11

RESULT 90
AX471729
LOCUS AX471729 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1306 from Patent WO02053773.
ACCESSION AX471729
VERSION AX471729.1 GI:22206854
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Hofmann, K., Conradt, M. and Petersohn, D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1306 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
Db 2 TGGCAGGCAC 11

RESULT 91
AX623912/c
LOCUS AX623912 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 953 from Patent WO02053774.
ACCESSION AX623912
VERSION AX623912.1 GI:28451853
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Petersohn, D., Conradt, M. and Hofmann, K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 953 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGGC 14
Db 10 ACTGCTGGC 1

RESULT 92
AX624033
LOCUS AX624033 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1074 from Patent WO02053774.
ACCESSION AX624033
VERSION AX624033.1 GI:28451974
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Petersohn, D., Conradt, M. and Hofmann, K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1074 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGGCAC 20
Db 2 TGGCAAGCAC 11

RESULT 93
AX624211
LOCUS AX624211 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1252 from Patent WO02053774.
ACCESSION AX624211
VERSION AX624211.1 GI:28452152
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1252 11-JUL-2002; (DE)
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
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Db 2 TGGCAGCGC 11

RESULT 94
AX624372
LOCUS AX624372 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1413 from Patent WO02053774.
ACCESSION AX624372
VERSION AX624372.1 GI:28452313
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1413 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/mol_type="unassigned DNA"
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 95
AX624551
LOCUS AX624551 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1592 from Patent WO02053774.
ACCESSION AX624551
VERSION AX624551.1 GI:28452492
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1592 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 96
AX626287
LOCUS AX626287 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3328 from Patent WO02053774.
ACCESSION AX626287
VERSION AX626287.1 GI:28454325
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3328 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 97
AX626311
LOCUS AX626311 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3352 from Patent WO02053774.
ACCESSION AX626311
VERSION AX626311.1 GI:28454349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3352 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 98
AX626311
LOCUS AX626311 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3352 from Patent WO02053774.
ACCESSION AX626311
VERSION AX626311.1 GI:28454349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3352 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCTGGCAGCGC 18
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Db 1 GCTGGCAGCGC 10
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1252 11-JUL-2002; (DE)
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 96
AX626287
LOCUS AX626287 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3328 from Patent WO02053774.
ACCESSION AX626287
VERSION AX626287.1 GI:28454325
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3328 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGC 20
| | | | |
Db 2 TGGCAGCGC 11

RESULT 97
AX626311
LOCUS AX626311 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3352 from Patent WO02053774.
ACCESSION AX626311
VERSION AX626311.1 GI:28454349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3352 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCTGGCAGCGC 18
| | | | |
Db 1 GCTGGCAGCGC 10
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RESULT 98
AX629490/c
LOCUS      AX629490      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6531 from Patent WO02053774.
ACCESSION  AX629490
VERSION     AX629490.1  GI:28457528
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8375 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 TGGCAGCGAC 20
Db      10 TGGCAGGAC 1

            |||||
            |||||

RESULT 99
AX629976
LOCUS      AX629976      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7017 from Patent WO02053774.
ACCESSION  AX629976
VERSION     AX629976.1  GI:28458014
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7017 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 TGGCAGCGAC 20
Db      10 TGGCAGGAC 1

            |||||
            |||||

RESULT 100
AX631333/c
LOCUS      AX631333      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8375 from Patent WO02053774.
ACCESSION  AX631333
VERSION     AX631333.1  GI:28459379
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8375 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GGACTCGCTG 12
Db      2 GGACTCCTG 11

            |||||
            |||||

RESULT 101
AX631454
LOCUS      AX631454      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8496 from Patent WO02053774.
ACCESSION  AX631454
VERSION     AX631454.1  GI:28459520
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8496 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 ACTCGCTGGC 14
Db      10 ACTGGCTGGC 1

            |||||
            |||||

RESULT 102
AX631632
LOCUS      AX631632      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8674 from Patent WO02053774.
ACCESSION  AX631632
VERSION     AX631632.1  GI:28459708
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8674 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 TGGCAGCGAC 20
Db      2 TGGCAAGCAC 11

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            |||||

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Query Match          42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGAC 20
    |||||
Db 2 TGGCAGCGC 11

RESULT 103
AX631793
LOCUS
DEFINITION Sequence 8835 from Patent WO02053774.
ACCESSION AX631793
VERSION AX631793.1 GI:28459900
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8835 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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            /db_xref="taxon:9606"

Query Match          42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGAC 20
    |||||
Db 2 TGGCAGCGC 11

RESULT 104
AX631972
LOCUS
DEFINITION Sequence 9014 from Patent WO02053774.
ACCESSION AX631972
VERSION AX631972.1 GI:28467587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9014 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
    source
        1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match          42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGAC 20
    |||||
Db 2 TGGCAGCGC 11

RESULT 105
AX631972
LOCUS
DEFINITION Sequence 9014 from Patent WO02053774.
ACCESSION AX631972
VERSION AX631972.1 GI:28467587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9014 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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        1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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Query Match          42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCGAC 20
    |||||
Db 2 TGGCAGCGC 11

RESULT 105
BD091223
LOCUS
DEFINITION Hetero dimer fused proteins useful against targeting immunotherapy
          and General immunostimulation.
ACCESSION BD091223
VERSION BD091223.1 GI:22636833
KEYWORDS JP 2001525423-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Gillies,S.D., Lo,K.M. and Lan,Y.
          Hetero dimer fused proteins useful against targeting immunotherapy
          and general immunostimulation
          Patent: JP 2001525423-A 8 11-DEC-2001;
          LEXIGEN PHARMACEUTICALS CORP
JOURNAL OS Artificial Sequence
COMMENT PN JP 2001525423-A/8
          PD 11-DEC-2001
          PF 08-DEC-1998 JP 2000524321
          PP 08-DEC-1997 US 08/986997
          PI STEPHEN D GILLIES,KIN MING LO,YAN LAN
          PC C07K19/00,A61K47/48,A61P37/04,C07K14/54,C07K16/30,C12N15/09,
          C12P21/00//
          PC A61K39/00,C12N15/00,A61K37/02
          PC A61K39/00,C12N15/00,A61K37/02
          CC Description of Artificial Sequence: Synthetic Oligonucleotide
          FH Key Location/Qualifiers
          FT source
              1..11
                  /organism="Artificial Sequence".
          FT Location/Qualifiers
              1..11
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"

Query Match          42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCGC 10
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Db 2 ATGGACTTGC 11

RESULT 106
BD234977
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234977
VERSION BD234977.1 GI:33044747
KEYWORDS JP 2002517434-A/81.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 81 18-JUN-2002;
          BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MEH
COMMENT OS Homo sapiens (human)
          PN JP 2002517434-A/81
          PD 18-JUN-2002
          PF 10-JUN-1999 JP 2000553044
          PP 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
          KARL HERMANN SCHLINGENSIEPEN,REINAR SCHLINGENSIEPEN,WOLFGANG PI
          BRYSCH
          PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
          PC 00,A61P35/00,
          PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
          method for stimulating the immune system
          FH Key Location/Qualifiers
          FT source
              1..12
                  /organism="Homo sapiens (human)".

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FEATURES
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        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCTGG 13
Db 3 GAGTCGCTGG 12

RESULT 107
AX009048
LOCUS AX009048 12 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 81 from Patent WO9963975.
ACCESSION AX009048
VERSION AX009048.1 GI:9996422
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 81 16-DEC-1999;
BIOLOGISTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
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    Location/Qualifiers
      1..12
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 42.0%; Score 8.4; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GACTCGCTGG 13
Db 3 GAGTCGCTGG 12

RESULT 108
AX767991/c
LOCUS AX767991 9 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 1 from Patent WO0304225.
ACCESSION AX767991
VERSION AX767991.1 GI:32436671
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gehrmann,M., Schweser,S. and Weidner,M.
TITLE Profiling of the immune gene repertoire
JOURNAL Patent: WO 0304225-A 1 30-MAY-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
  source
    Location/Qualifiers
      1..9
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 9;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
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      1..10
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        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 100.0%; Pred. No. 80;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCAC 16
Db 9 GCTGGCAC 2

RESULT 109
A52274/c
LOCUS A52274 10 bp DNA linear PAT 12-DEC-1997
DEFINITION Sequence 64 from Patent EP0705842.
ACCESSION A52274
VERSION A52274.1 GI:2852038
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Bartnik,E.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-beta
JOURNAL Patent: EP 0705842-A 64 10-APR-1996;
HOECHST AG (DE)
COMMENT Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 110
A91804/c
LOCUS A91804 10 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 3 from Patent WO9823775.
ACCESSION A91804
VERSION A91804.1 GI:6740684
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nees M. and Duerst, M.
TITLE DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL Patent: WO 9823775-A 3 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
FEATURES
  source
    Location/Qualifiers
      1..10
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 100.0%; Pred. No. 80;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 111
A97598/c
LOCUS A97598 10 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 4 from Patent WO9915880.

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ACCESSION A97598
 VERSION A97598.1 GI:6780901
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Roberts,J.A. and Paul,W.
 TITLE CONTROL OF PLANT ABSCISSION AND POD DEHISCENCE OR SHATTER
 JOURNAL PATENT: WO 9915680-A 4 01-APR-1999;
 BIOGEMMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
 FEATURES Location/Qualifiers
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 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.80;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 112
 AR016246/c
 LOCUS AR016246 10 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 14 from patent US 5776683.
 ACCESSION AR016246
 VERSION AR016246.1 GI:3972523
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Smith,H.S. and Chen,L.-C.
 TITLE Methods for identifying genes amplified in cancer cells
 JOURNAL PATENT: US 5776683-A 14 07-JUL-1998;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.80;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 113
 AR044027/c
 LOCUS AR044027 10 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5817461.
 ACCESSION AR044027
 VERSION AR044027.1 GI:5965492
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Austin,R.C., Hirsch,J. and Weitz,J.I.
 TITLE Methods and compositions for diagnosis of hyperhomocysteinemia
 JOURNAL PATENT: US 5817461-A 4 06-OCT-1998;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.80;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 114
 AR079092/c
 LOCUS AR079092 10 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 13 from patent US 5965409.
 ACCESSION AR079092
 VERSION AR079092.1 GI:10005838
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Pardee,A.B. and Liang,P.
 TITLE System for comparing levels or amounts of mRNAs
 JOURNAL PATENT: US 5965409-A 13 12-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.80;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
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 Db 9 TCGCTGGC 2

RESULT 115
 AR079528/c
 LOCUS AR079528 10 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 3 from patent US 5965707.
 ACCESSION AR079528
 VERSION AR079528.1 GI:10006272
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Tam,S.-Y., Tsai,M. and Galli,S.J.
 TITLE Rin2, a novel inhibitor of Ras-mediated signaling
 JOURNAL PATENT: US 5965707-A 3 12-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.80;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGGC 14
 |||||
 Db 9 TCGCTGGC 2

RESULT 116
 AR099718/c
 LOCUS AR099718 10 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 28 from patent US 6077948.
 ACCESSION AR099718
 VERSION AR099718.1 GI:12809484
 KEYWORDS
 SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
  Russell, M.B. and Utans, U.
  Mediators of chronic allograft rejection (AIF-1) and DNA encoding
  them
JOURNAL Patent: US 6077948-A 28 JUN-2000;
FEATURES
  source
    Location/Qualifiers
    1..10
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 117
LOCUS AR113051/c 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6132965.
ACCESSION AR113051
VERSION AR113051.1 GI:14093373
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
  Austin, R.C., Hirsch, J. and Weitz, J.I.
  Methods and compositions for diagnosis of hyperhomocysteinemia
  Patent: US 6132965-A 4 17-OCT-2000;
JOURNAL Location/Qualifiers
FEATURES
  source
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      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 118
LOCUS AR167221/c 10 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 55 from patent US 6284466.
ACCESSION AR167221
VERSION AR167221.1 GI:16243735
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
  Benson, A.
  Method of detecting genetic polymorphisms using over represented
  sequences
JOURNAL Patent: US 6284466-A 55 04-SEP-2001;
FEATURES
  source
    Location/Qualifiers
    1..10
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 8 CGCTGGCA 15
Db 9 CGCTGGCA 2

RESULT 119
LOCUS BD239869/c 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239869
VERSION BD239869.1 GI:33049639
KEYWORDS JP 2002534056-A/1287.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
  Roberts, B.L. and Shankara, S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 1287 15-OCT-2002;
JOURNAL GENZYME CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002534056-A/1287
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
  19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
  19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/080079 PR
  19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
  19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
  19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
  19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR
  19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
  19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
  19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR
  19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR
  19-JUN-1998 US 60/089994, 19-JUN-1998 US 60/090077 PR
  19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
  19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
  08-DEC-1998 US 60/111715
  PI BRUCE L ROBERTS, SRINIVAS SHANKARA
  PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
  C12N1/19,
  G01N37/00, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
  G01N37/00,
  CC C12N15/00, C12N5/00, C12N15/00
  CC Preparation and use of superior vaccines
  FH Key
  FT source
    1..10
      /organism="Homo sapiens (human)"
FEATURES
  source
    Location/Qualifiers
    1..10
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGACTCG 9
Db 10 TGGACTCG 3

RESULT 120
LOCUS BD240506 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240506
VERSION BD240506.1 GI:33050276
KEYWORDS JP 2002534056-A/1924.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1924 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1924
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089894,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TGGCAGCG 18
| | | | |
Db 2 TGGCAGCG 9
RESULT 121
BD248338/c
LOCUS BD248338 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Tobacco-origin novel salicylic acid-inducible gene and promoter.
ACCESSION BD248338
VERSION BD248338.1 GI:33058108
KEYWORDS JP 2002524051-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stuijver,M.H., Jepson,I., Horvath,D.M. and Chua,N.H.
TITLE Tobacco-origin novel salicylic acid-inducible gene and promoter
JOURNAL Patent: JP 2002524051-A 14 06-AUG-2002;
SYNGENTA MOGEN BV
COMMENT OS Artificial Sequence
PN JP 2002524051-A/14
PD 06-AUG-2002
PF 02-AUG-1999 JP 2000563809
PR 03-AUG-1998 US 60/095187
PI MAARTEN HENDRIK STUIJVER, IAN JEPSON, DIANA MEREDITH HORVATH, NAM

PI HAI CHUA
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
Description of Artificial Sequence Primer AP1 FH Key
Location/Qualifiers 1..10
FT source /organism='Artificial Sequence'.
FEATURES
source
1..10
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 TCGCTGGC 14
| | | | |
Db 9 TCGCTGGC 2
RESULT 122
I22447/c
LOCUS I22447 10 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 28 from patent US 5527884.
ACCESSION I22447
VERSION I22447.1 GI:1602801
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Russell,M.E. and Utans,U.
TITLE Mediators of chronic allograft rejection and DNA molecules encoding them
JOURNAL Patent: US 5527884-A 28 18-JUN-1996;
FEATURES
source
1..10
Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 TCGCTGGC 14
| | | | |
Db 9 TCGCTGGC 2
RESULT 123
I34793/c
LOCUS I34793 10 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 13 from patent US 559672.
ACCESSION I34793
VERSION I34793.1 GI:2087761
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Liang,P., Pardee,A.B. and Bianchi,C.F.
TITLE Method of differential display of exposed mRNA by RT/PCR
JOURNAL Patent: US 559672-A 13 04-FEB-1997;
FEATURES
source
1..10
Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 124
I64511/c
LOCUS I64511 10 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 13 from patent US 5665547.
ACCESSION I64511
VERSION I64511.1 GI:2481405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 10)
  Pardee,A.B. and Liang,P.
  Methods of comparing levels or amounts of mRNAs
  Patent: US 5665547-A 13 09-SEP-1997;
  Location/Qualifiers
  1..10
  /organism="unknown"
  /mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 125
AR238724/c
LOCUS AR238724 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 132 from patent US 6468743.
ACCESSION AR238724
VERSION AR238724.1 GI:27283794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 10)
  Romick,T.L. and Fraser,M.S.
  PCR techniques for detecting microbial contaminants in foodstuffs
  Patent: US 6468743-A 132 22-OCT-2002;
  Location/Qualifiers
  1..10
  /organism="unknown"
  /mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 126
AR270938/c
LOCUS AR270938 10 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6500942.
ACCESSION AR270938
VERSION AR270938.1 GI:29702188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 10)
  Tam,S.-Y., Tsai,M. and Galli,S.J.

```

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TITLE Rin2, a novel inhibitor of Ras-mediated signaling
JOURNAL Patent: US 6500942-A 3 31-DEC-2002;
FEATURES
  source
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  /organism="unknown"
  /mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 127
AX016299/c
LOCUS AX016299 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO949046.
ACCESSION AX016299
VERSION AX016299.1 GI:10041862
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
  1
  Roberts,J.A., Wyatt,P. and Whitelaw,C.
  Signal transduction protein involved in plant dehiscence
  Patent: WO 9949046-A 2 30-SEP-1999;
  ROBERTS JEREMY ALAN (GB); BIOGENMA UK LTD (GB); WYATT PAUL (GB);
  WHITELAW CATHERINE (GB)
  Location/Qualifiers
  1..10
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Arbitrary primer A"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTGGC 14
Db 9 TCGCTGGC 2

RESULT 128
AX152168
LOCUS AX152168 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 83 from Patent WO0138577.
ACCESSION AX152168
VERSION AX152168.1 GI:14533819
KEYWORDS
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1
  Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Human transcriptomes
  Patent: WO 0138577-A 83 31-MAY-2001;
  The Johns Hopkins University (US)
  Location/Qualifiers
  1..10
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible][illegible]

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REFERENCE 1 (bases 1 to 11)
AUTHORS Chee,M.S.
TITLE Computer-aided visualization and analysis system for sequence
evaluation
JOURNAL Patent: US 5795716-A 39 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..11
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 133
AR082679
LOCUS AR082679 11 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 39 from patent US 5974164.
ACCESSION AR082679
VERSION AR082679.1 GI:10009399
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Chee,M.S.
TITLE Computer-aided visualization and analysis system for sequence
evaluation
JOURNAL Patent: US 5974164-A 39 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 134
AR156206
LOCUS AR156206 11 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 39 from patent US 6242180.
ACCESSION AR156206
VERSION AR156206.1 GI:15124910
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Chee,M.S.
TITLE Computer-aided visualization and analysis system for sequence
evaluation
JOURNAL Patent: US 6242180-A 39 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..11
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 135
AR381088
LOCUS AR381088 11 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 39 from patent US 6607887.
ACCESSION AR381088
VERSION AR381088.1 GI:40088812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Chee,M.S.
TITLE Computer-aided visualization and analysis system for sequence
evaluation
JOURNAL Patent: US 6607887-A 39 19-AUG-2003;
FEATURES Location/Qualifiers
source 1..11
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 137
AX470788/c
LOCUS AX470788 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 365 from Patent WO02053773.
ACCESSION AX470788
VERSION AX470788.1 GI:22205913
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 135
AR301731/c
LOCUS AR301731 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 312 from patent US 6538173.
ACCESSION AR301731
VERSION AR301731.1 GI:31689533
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 312 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..11
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGCACGCA 19
Db 11 GGCACGCA 4

RESULT 136
AR381088
LOCUS AR381088 11 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 39 from patent US 6607887.
ACCESSION AR381088
VERSION AR381088.1 GI:40088812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Chee,M.S.
TITLE Computer-aided visualization and analysis system for sequence
evaluation
JOURNAL Patent: US 6607887-A 39 19-AUG-2003;
FEATURES Location/Qualifiers
source 1..11
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGGCAGC 17
Db 1 CTGGCAGC 8

RESULT 137
AX470788/c
LOCUS AX470788 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 365 from Patent WO02053773.
ACCESSION AX470788
VERSION AX470788.1 GI:22205913
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Query Match	40.0%; Score 8; DB 1;	Length 11;			
Best Local Similarity	100.0%; Pred. No. 89;				
Matches	8; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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QY	13 GCAGGCAC 20				
Db	11 GCAGGCAC 4				
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RESULT 140					
AX471851/c					PAT 09-AUG-2002
LOCUS	AX471851	11 bp	DNA	linear	
DEFINITION	Sequence 1428 from Patent WO02053773.				
ACCESSION	AX471851				
VERSION	AX471851.1 GI:22206976				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Hofmann K., Conradt M. and Petersohn D.				
TITLE	Method for determining skin stress or skin ageing in vitro				
JOURNAL	Patent: WO 02053773-A 1428 11-JUL-2002;				
FEATURES	HENKEL KGAA (DE)				
source	Location/Qualifiers				
	1..11				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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Query Match	40.0%; Score 8; DB 1;	Length 11;			
Best Local Similarity	100.0%; Pred. No. 89;				
Matches	8; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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QY	1 ATGGACTC 8				
Db	11 ATGGACTC 4				
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RESULT 141					
AX623074					PAT 21-FEB-2003
LOCUS	AX623074	11 bp	DNA	linear	
DEFINITION	Sequence 115 from Patent WO02053774.				
ACCESSION	AX623074				
VERSION	AX623074.1 GI:28451015				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Petersohn D., Conradt M. and Hofmann K.				
TITLE	Method for determining homeostasis of the skin				
JOURNAL	Patent: WO 02053774-A 115 11-JUL-2002;				
FEATURES	Henkel Kommanditgesellschaft auf Aktien (DE)				
source	Location/Qualifiers				
	1..11				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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Query Match	40.0%; Score 8; DB 1;	Length 11;			
Best Local Similarity	100.0%; Pred. No. 89;				
Matches	8; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
<hr/>					
QY	11 TGGCACGC 18				
Db	2 TGGCACGC 9				
<hr/>					
RESULT 142					

LOCUS AX624694 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1735 from Patent WO02053774.
ACCESSION AX624694
VERSION AX624694.1 GI:28452635
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1735 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db 11 GCACGCAC 4
RESULT 143
AX624914
LOCUS AX624914 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1955 from Patent WO02053774.
ACCESSION AX624914
VERSION AX624914.1 GI:28452855
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1955 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TGGCAGCG 18
Db 1 TGGCAGCG 8
RESULT 144
AX625058/c
LOCUS AX625058 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2099 from Patent WO02053774.
ACCESSION AX625058
VERSION AX625058.1 GI:28452999
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2099 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 GCACGCAC 20
Db 11 GCACGCAC 4
RESULT 145
AX625700/c
LOCUS AX625700 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2741 from Patent WO02053774.
ACCESSION AX625700
VERSION AX625700.1 GI:28453641
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTC 8
Db 8 ATGGACTC 1
RESULT 146
AX625812
LOCUS AX625812 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2853 from Patent WO02053774.
ACCESSION AX625812
VERSION AX625812.1 GI:28453753
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2853 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACTC 8
Db 8 ATGGACTC 1

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCAC 16
| | | | | | | |
Db 3 GCTGGCAC 10

RESULT 147
AX628487/c
LOCUS AX628487 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5528 from Patent WO02053774.
ACCESSION AX628487
VERSION AX628487.1 GI:28456525
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5528 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCGCTGG 13
| | | | | | | |
Db 11 CTCGCTGG 4

RESULT 148
AX628761/c
LOCUS AX628761 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5802 from Patent WO02053774.
ACCESSION AX628761
VERSION AX628761.1 GI:28456799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5802 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCACGCA 19
| | | | | | | |
Db 11 GGCACGCA 4

RESULT 149
AX629639/c
LOCUS AX629639 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6680 from Patent WO02053774.

ACCESSION AX629639
VERSION AX629639.1 GI:28457677
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6680 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8
| | | | | | | |
Db 10 ATGGACTC 3

RESULT 150
AX629743
LOCUS AX629743 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6784 from Patent WO02053774.
ACCESSION AX629743
VERSION AX629743.1 GI:28457781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6784 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTCG 9
| | | | | | | |
Db 3 TGGACTCG 10

RESULT 151
AX630495
LOCUS AX630495 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7536 from Patent WO02053774.
ACCESSION AX630495
VERSION AX630495.1 GI:28458533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7536 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source

1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 18

Db 2 TGGCAGC 9

RESULT 152

AX632115/c

LOCUS

DEFINITION Sequence 9157 from Patent WO02053774.

ACCESSION AX632115

VERSION AX632115.1 GI:28467730

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 9157 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source

1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 40.0%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20

Db 11 GCACGCAC 4

RESULT 153

AX632335

LOCUS

DEFINITION Sequence 9377 from Patent WO02053774.

ACCESSION AX632335

VERSION AX632335.1 GI:28467950

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 9377 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source

1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 40.0%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 18

Db 2 TGGCAGC 9

QY 11 TGGCAGC 18

Db 1 TGGCAGC 8

RESULT 154

AX632479/c

LOCUS

DEFINITION Sequence 9521 from Patent WO02053774.

ACCESSION AX632479

VERSION AX632479.1 GI:28468094

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 9521 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

Location/Qualifiers

source

1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 40.0%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCAC 20

Db 11 GCACGCAC 4

RESULT 155

AX632794/c

LOCUS

DEFINITION Sequence 9836 from Patent WO02053774.

ACCESSION AX632794

VERSION AX632794.1 GI:28468409

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 9836 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

Location/Qualifiers

source

1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 40.0%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACTC 8

Db 11 ATGGACTC 4

RESULT 156

AX632796/c

LOCUS

DEFINITION Sequence 9838 from Patent WO02053774.

ACCESSION AX632796

VERSION AX632796.1 GI:28468411

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 9838 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

Location/Qualifiers

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE     1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS       Method for determining homeostasis of the skin
TITLE         Patent: WO 02053774-A 9838 11-JUL-2002;
JOURNAL       Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
source        1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match   40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           13 GCACGCAC 20
Db           11 GCACGCAC 4

RESULT 157
BD124481/c
LOCUS        BD124481 11 bp DNA linear PAT 18-SEP-2002
DEFINITION   Compositions and method for healing wound.
ACCESSION    BD124481
VERSION      BD124481.1 GI:23219426
KEYWORDS     JP 2002503460-A/312.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE         Katz,E.H.
JOURNAL       1 (bases 1 to 11)
COMMENT      Compositions and method for healing wound
PATENT: JP 2002503460-A 312 05-FEB-2002;
THE WISTAR INSTITUTE
OS           Mus musculus (mouse)
PN           JP 2002503460-A/312
PD           05-FEB-2002
PF           12-FEB-1999 JP 2000531545
PR           13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
PS           28-SEP-1998 US 60/102051
PT           ELLEN HEBER KATZ
PC           C12N15/09,A01K67/027,C12N5/10,C12Q1/69,G01N33/50,C12N15/00, PC
C12N5/00
CC           Compositions and method for healing wound
FH           Location/Qualifiers
FT           1..11
FT           source 1..11
FEATURES      Location/Qualifiers
source        1..11
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /db_xref="taxon:10090"
Query Match   40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           12 GCACGCAC 19
Db           11 GCACGCAC 4

RESULT 158
ARI35803
LOCUS        ARI35803 12 bp DNA linear PAT 16-JUN-2001
DEFINITION   Sequence 5 from patent US 6136568.

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ACCESSION    ARI35803
VERSION      ARI35803.1 GI:14476475
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Hiatt,A.C. and Rose,F.D.
TITLE         De novo polynucleotide synthesis using rolling templates
JOURNAL       Patent: US 6136568-A 5 24-OCT-2000;
FEATURES      Location/Qualifiers
source        1..12
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   40.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 98;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           1 ATGGACTC 8
Db           5 ATGGACTC 12

RESULT 159
ARI68866/c
LOCUS        ARI68866 11 bp DNA linear PAT 17-DEC-2001
DEFINITION   Sequence 8 from patent US 6288142.
ACCESSION    ARI68866
VERSION      ARI68866.1 GI:17905009
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE     1 (bases 1 to 11)
AUTHORS       Eugon,P. and Herren,F.
TITLE         Process for warp-free pigmenting of polyolefins
JOURNAL       Patent: US 6288142-A 8 11-SEP-2001;
FEATURES      Location/Qualifiers
source        1..11
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches       9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy           8 CGCTGCACGC 18
Db           11 CGCGGCGCGC 1

RESULT 160
ARI6095/c
LOCUS        I16095 11 bp DNA linear PAT 03-APR-1996
DEFINITION   Sequence 4 from patent US 5474897.
ACCESSION    I16095
VERSION      I16095.1 GI:1251003
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE     1 (bases 1 to 11)
AUTHORS       Weiss,A. and Fraser,J.
TITLE         Screening assay for the identification of novel immunosuppressives
JOURNAL       Patent: US 5474897-A 4 12-DEC-1995;
FEATURES      Location/Qualifiers
source        1..11
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   39.0%; Score 7.8; DB 1; Length 11;

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Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
Db 11 TGGAACTCTG 1

RESULT 161
AX319383/c
LOCUS AX319383 11 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 55 from Patent WO0172783.
ACCESSION AX319383
VERSION AX319383.1 GI:17901170
KEYWORDS
SOURCE Hypocrea jecorina
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE
1
AUTHORS Penttila,M.E., Ward,M., Wang,H., Valkonen,M.J. and Saloheimo,M.L.
TITLE Production of secreted proteins by recombinant eukaryotic cells.
JOURNAL Patent: WO 0172783-A 55 04-OCT-2001;
GENENCOR INTERNATIONAL, INC. (US)

FEATURES
source
1. .11
Location/Qualifiers
/organism="Hypocrea jecorina"
/mol_type="unassigned DNA"
/db_xref="taxon:51453"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGCG 14
Db 11 GACACGTGGC 1

RESULT 162
AX470747
LOCUS AX470747 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470747
VERSION AX470747.1 GI:22205872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 324 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
Db 1 TGGCCCTCTCTG 11

RESULT 163
AX471766
LOCUS AX471766 11 bp DNA linear PAT 09-AUG-2002

Sequence 1343 from Patent WO02053773.
AX471766
AX471766.1 GI:22206891
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1343 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGCG 14
Db 1 GACCAGCTGGC 11

RESULT 164
AX623493
LOCUS AX623493 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 534 from Patent WO02053774.
ACCESSION AX623493
VERSION AX623493.1 GI:28451434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 534 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACTCGCTGCG 14
Db 1 GTCTCGCTGAC 11

RESULT 165
AX623691
LOCUS AX623691 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 732 from Patent WO02053774.
ACCESSION AX623691
VERSION AX623691.1 GI:28451632
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 732 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGCAC 16
DB 1 CTCACAGGCAC 11

RESULT 166
AX624406/c

LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1447 from Patent WO02053774.
ACCESSION AX624406
VERSION AX624406.1 GI:28452347
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1447 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
DB 11 GCTGGGAGCA 1

RESULT 167
AX624475/c

LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1516 from Patent WO02053774.
ACCESSION AX624475
VERSION AX624475.1 GI:28452416
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1516 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCTGGCAGCA 19
DB 11 GCTGGGAGCA 1

RESULT 168
AX626034

LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3075 from Patent WO02053774.
ACCESSION AX626034
VERSION AX626034.1 GI:28454072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3075 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 1 TGGCCTCTCTG 11

RESULT 169
AX626284

LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3325 from Patent WO02053774.
ACCESSION AX626284
VERSION AX626284.1 GI:28454322
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3325 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
DB 1 TGGCCTCTCTG 11

RESULT 170
AX627660/c

LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4701 from Patent WO02053774.
ACCESSION AX627660

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VERSION      AX627660.1  GI:28455698
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4701 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      2  TGGACTCGCTG 12
          |||||
  Db      11  TGAATCACTG 1

RESULT 171
AX627817/c
LOCUS      AX627817
DEFINITION Sequence 4858 from Patent WO02053774.
ACCESSION AX627817
VERSION    AX627817.1  GI:28455695
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4858 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      10  CTGGCAGCGAC 20
           |||||
  Db      11  CTGGCAGTCAC 1

RESULT 172
AX629160
LOCUS      AX629160
DEFINITION Sequence 6201 from Patent WO02053774.
ACCESSION AX629160
VERSION    AX629160.1  GI:28457198
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6201 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)

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    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      4  GACTCGCTGCG 14
          |||||
  Db      1  GACAGGCTGGC 11

RESULT 173
AX630914
LOCUS      AX630914
DEFINITION Sequence 7955 from Patent WO02053774.
ACCESSION AX630914
VERSION    AX630914.1  GI:28458954
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7955 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      4  GACTCGCTGCG 14
          |||||
  Db      1  GTCTCGCTGAC 11

RESULT 174
AX631112
LOCUS      AX631112
DEFINITION Sequence 8153 from Patent WO02053774.
ACCESSION AX631112
VERSION    AX631112.1  GI:28459156
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8153 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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  1. .11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      4  GACTCGCTGCG 14
          |||||
  Db      1  GTCTCGCTGAC 11

RESULT 175
AX631112
LOCUS      AX631112
DEFINITION Sequence 8153 from Patent WO02053774.
ACCESSION AX631112
VERSION    AX631112.1  GI:28459156
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8153 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match      39.0%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 99;
  Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      6  CTCGCTGCGAC 16

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Db      1 CTCACAGGCAC 11
|||||
RESULT 175
AX631827/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8869 from Patent WO02053774.
ACCESSION AX631827
VERSION    AX631827.1 GI:28459934
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES     Petersohn,D., Conradt,M. and Hofmann,K.
JOURNAL    Method for determining homeostasis of the skin
PATENT: WO 02053774-A 8869 11-JUL-2002;
JOURNAL    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 GCTGGCAGCA 19
|||||
Db      11 GCTGGGAGCA 1

RESULT 176
AX631896/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8938 from Patent WO02053774.
ACCESSION AX631896
VERSION    AX631896.1 GI:28460034
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES     Petersohn,D., Conradt,M. and Hofmann,K.
JOURNAL    Method for determining homeostasis of the skin
PATENT: WO 02053774-A 8938 11-JUL-2002;
JOURNAL    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGACTCGCTG 12
|||||
Db      11 TGGTCTCGGTG 1

RESULT 177
A06190/c
LOCUS      12 bp      DNA      linear      PAT 04-JUN-1993
DEFINITION Part linker.
ACCESSION A06190
VERSION    A06190.1 GI:411222
KEYWORDS

SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE   1 (bases 1 to 12)
TITLES     GENE MODIFICATION
JOURNAL    Patent: WO 9001549-A 18 22-FEB-1990;
FEATURES   Location/Qualifiers
source     1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GACTCGCTGGC 14
|||||
Db      11 GACTCGGGCC 1

RESULT 178
A61480
LOCUS      12 bp      DNA      linear      PAT 09-MAR-1998
DEFINITION Sequence 49 from Patent WO9710332.
ACCESSION A61480
VERSION    A61480.1 GI:3715875
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1
AUTHORS    Schmidt,G.
TITLES     CHIMAERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
JOURNAL    OF ANTISENSE BINDING SITES
PATENT: WO 9710332-A 49 20-MAR-1997;
JOURNAL    BRAX GENOMICS LTD (GB)
FEATURES   Location/Qualifiers
source     1..12
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 GCTGGCAGCA 19
|||||
Db      2 GCTGCCAGCA 12

RESULT 179
A71519/c
LOCUS      12 bp      DNA      linear      PAT 07-MAY-1999
DEFINITION Sequence 78 from Patent WO9813521.
ACCESSION A71519
VERSION    A71519.1 GI:4775131
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1 (bases 1 to 12)
AUTHORS    Fesce,R. and Consalez,G.
TITLES     METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
JOURNAL    PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
PATENT: WO 9813521-A 78 02-APR-1998;
JOURNAL    FESCE RICCARDO (IT)
FEATURES   Location/Qualifiers
source     1..12
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            /mol_type="unassigned DNA"

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/db_xref="taxon:32644"

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACTCGCTGG 13
 Db 11 GAACACGCTGG 1

RESULT 180
 LOCUS ARI00990 12 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 78 from patent US 6083693.
 ACCESSION ARI00990
 VERSION ARI00990.1 GI:12811788
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Nandabalan,K. and Rothberg,J.Marc.
 TITLE Identification and comparison of protein-protein interactions that occur in populations
 JOURNAL Patent: US 6083693-A 78 04-JUL-2000;
 FEATURES Location/Qualifiers
 source 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
 Db 1 TCGAGTCGCTG 11

RESULT 181
 LOCUS ARI00991 12 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 79 from patent US 6083693.
 ACCESSION ARI00991
 VERSION ARI00991.1 GI:12811789
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Nandabalan,K. and Rothberg,J.Marc.
 TITLE Identification and comparison of protein-protein interactions that occur in populations
 JOURNAL Patent: US 6083693-A 79 04-JUL-2000;
 FEATURES Location/Qualifiers
 source 1..12
 /organism="unknown"
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Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGACTCGCTG 12
 Db 1 TCGAGTCGCTG 11

RESULT 182
 LOCUS ARI00992 12 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 181 from patent US 6287769.

ACCESSION ARI67817
 VERSION ARI67817.1 GI:17903622
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Inoue,T.
 TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of assaying microorganisms, method of analyzing microorganisms and method of assaying contaminant
 JOURNAL Patent: US 6287769-A 181 11-SEP-2001;
 FEATURES Location/Qualifiers
 source 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCA 15
 Db 1 ACTGGCCGGCA 11

RESULT 183
 LOCUS E29701 12 bp DNA linear PAT 18-JUN-2001
 DEFINITION Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste.
 ACCESSION E29701
 VERSION E29701.1 GI:13021204
 KEYWORDS JP 1999276176-A/181.
 SOURCE unidentified
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Koichi, I.
 TITLE Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste
 JOURNAL Patent: JP 1999276176-A 181 12-OCT-1999;
 COMMENT SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
 OS Unidentified
 PN JP 1999276176-A/181
 PD 12-OCT-1999
 PF 31-MAR-1998 JP 1998087652
 PR KOICHI INOUE
 PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
 Strandedness: Single;
 PH Key Location/Qualifiers
 FT source 1..12
 /organism="Unidentified".
 FEATURES Location/Qualifiers
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 /organism="unidentified"
 /mol_type="Genomic DNA"
 /db_xref="taxon:32644"

Query Match 39.0%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACTCGCTGGCA 15
 Db 1 ACTGGCCGGCA 11

RESULT 184
 LOCUS E38907 12 bp DNA linear PAT 31-JAN-2002
 DEFINITION


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RESULT 189
AR371424      12 bp  DNA      linear      PAT 12-SEP-2003
LOCUS
DEFINITION   Sequence 79 from patent US 6395478.
ACCESSION   AR371424
VERSION     AR371424.1 GI:34608358
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 12)
AUTHORS    Nandabalan,K. and Rothberg,J.M.
TITLE      Identification and comparison of protein-protein interactions that
           occur in populations and identification of inhibitors of these
           interactors
JOURNAL     Patent: US 6395478-A 79 28-MAY-2002;
FEATURES
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    1..12
    /location=Qualifiers
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGACTCGCTG 12
DB      1 TGCAGTCGCTG 11

RESULT 189
AX098966/c
LOCUS
DEFINITION   Sequence 29 from Patent WO0120026.
ACCESSION   AX098966
VERSION     AX098966.1 GI:13538176
KEYWORDS
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM

REFERENCE   1
AUTHORS    Wojnowski,L. and Hustert,E.
TITLE      Polymorphisms in the human hpvr gene and their use in diagnostic
           and therapeutic applications
JOURNAL     Patent: WO 0120026-A 29 22-MAR-2001;
           Epidaurus Biotechnologie AG (DE)
FEATURES
  source
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    /location=Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="artificial sequence"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 ACTCGTGGCA 15
DB      11 AGTCCCTGGCA 1

RESULT 190
AX136991/c
LOCUS
DEFINITION   Sequence 65 from Patent EP1088900.
ACCESSION   AX136991
VERSION     AX136991.1 GI:14273338
KEYWORDS
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM

REFERENCE   1
AUTHORS    Lyamichev,V., Skrzypczynski,Z., Allawi,H.T., Wayland,S.R., Takova,T.
           and Neri,B.P.
TITLE      Charge tags and separation of nucleic acid molecules
JOURNAL     Patent: WO 0206303-A 57 15-AUG-2002;
           THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
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    /location=Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"

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REFERENCE
AUTHORS    Hustert,E., Wojnowski,L. and Eiselt,R.
TITLE      Polymorphisms in the human cyp3a4, cyp3a7 and hpvr genes and their
           use in diagnostic and therapeutic applications
JOURNAL     Patent: EP 1088900-A 65 04-APR-2001;
           Epidaurus Biotechnologie AG (DE)
FEATURES
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    1..12
    /location=Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="DNA"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 ACTCGTGGCA 15
DB      11 AGTCCCTGGCA 1

RESULT 191
AX350140/c
LOCUS
DEFINITION   Sequence 663 from Patent WO202606.
ACCESSION   AX350140
VERSION     AX350140.1 GI:18615818
KEYWORDS
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM

REFERENCE   1
AUTHORS    Ratti,G. and Grandi,G.
TITLE      Immunisation against Chlamydia pneumoniae
JOURNAL     Patent: WO 0202606-A 663 10-JAN-2002;
           Chiron S.p.A. (IT)
FEATURES
  source
    1..12
    /location=Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Primer tail"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CTGGCAGGCAC 20
DB      11 CTAGTACGCAC 1

RESULT 192
AX698726
LOCUS
DEFINITION   Sequence 57 from Patent WO2063030.
ACCESSION   AX698726
VERSION     AX698726.1 GI:29499514
KEYWORDS
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM

REFERENCE   1
AUTHORS    Lyamichev,V., Skrzypczynski,Z., Allawi,H.T., Wayland,S.R., Takova,T.
           and Neri,B.P.
TITLE      Charge tags and separation of nucleic acid molecules
JOURNAL     Patent: WO 0206303-A 57 15-AUG-2002;
           THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
  source
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    /location=Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"

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/db_xref="taxon:32630"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGCTGGCAGC 18
   |||||
Db 1 CGCTGTCTGC 11

RESULT 193
BD105403
LOCUS      12 bp DNA linear PAT 27-AUG-2002
DEFINITION 5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same.
ACCESSION  BD105403
VERSION     BD105403.1 GI:22650977
KEYWORDS   JP 2001348398-A/3.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Saito,I., Fujimoto,K., Matsuda,S. and Yoshino,H.
TITLE     5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same
JOURNAL    JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    PN JP 2001348398-A/3
PD 18-DEC-2001
PF 05-JAN-2001 JP 2001000750
PI ISAO SAITO,KENZO FUJIMOTO,SHIGEO MATSUDA,HIDEAKI YOSHINO PC
C07H21/04,C07H1/00,C07H19/10,C12P19/30,C12Q1/68 CC Description of
Artificial Sequence:template DNA;named ODN C FH Key
Location/Qualifiers
FT source 1..12
/organism='Artificial Sequence'.

FEATURES
    source
        Location/Qualifiers
            1..12
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGC 16
   |||||
Db 1 CACGCGGCAC 11

RESULT 195
BD105407
LOCUS      12 bp DNA linear PAT 27-AUG-2002
DEFINITION 5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same.
ACCESSION  BD105407
VERSION     BD105407.1 GI:22650981
KEYWORDS   JP 2001348398-A/7.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Saito,I., Fujimoto,K., Matsuda,S. and Yoshino,H.
TITLE     5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same
JOURNAL    JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    PN JP 2001348398-A/7
PD 18-DEC-2001
PF 05-JAN-2001 JP 2001000750
PI ISAO SAITO,KENZO FUJIMOTO,SHIGEO MATSUDA,HIDEAKI YOSHINO PC
C07H21/04,C07H1/00,C07H19/10,C12P19/30,C12Q1/68 CC Description of
Artificial Sequence:template DNA;named ODN I PH Key
Location/Qualifiers
FT source 1..12
/organism='Artificial Sequence'.

FEATURES
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        Location/Qualifiers
            1..12
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCGCTGGCAGC 16
   |||||
Db 1 CACGCGGCAC 11

RESULT 196
AX668767
LOCUS      9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2216 from Patent WO0242459.
ACCESSION  AX668767
VERSION     AX668767.1 GI:29291742
KEYWORDS   JP 2001348398-A/4
SOURCE     synthetic construct
ORGANISM   synthetic construct

```

artificial sequences.

REFERENCE 1
 AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 2216 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 1..9
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="example target DNA"

source

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
 |||||
 Db 1 ATGGACTTG 9

RESULT 197

LOCUS AX668837 9 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 2286 from Patent WO0242459.
 ACCESSION AX668837
 VERSION AX668837.1 GI:29291812
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 2286 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 1..9

source

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
 |||||
 Db 1 ATGGACTTG 9

RESULT 198

LOCUS AX668838 9 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 2287 from Patent WO0242459.
 ACCESSION AX668838
 VERSION AX668838.1 GI:29291813
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 2287 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 1..9

source

/organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="example target DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGACTCG 9
 |||||
 Db 1 ATGGACTTG 9

RESULT 199

LOCUS AR000035 10 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 4 from patent US 5736294.
 ACCESSION AR000035
 VERSION AR000035.1 GI:3962566
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1

(bases 1 to 10)
 AUTHORS Ecker, D.J., Brice, T.W. and Vickers, T.A.
 TITLE Reagents and methods for modulating gene expression through RNA mimicry
 JOURNAL Patent: US 5736294-A 4 07-APR-1998;
 FEATURES Location/Qualifiers
 1..10
 source /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
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 Db 2 CTCCTGGC 10

RESULT 200

LOCUS AR020450 10 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 1 from patent US 5789160.
 ACCESSION AR020450
 VERSION AR020450.1 GI:3975065
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1

(bases 1 to 10)
 AUTHORS Eaton, B.E. and Gold, L.
 TITLE Parallel Selex
 JOURNAL Patent: US 5789160-A 1 04-AUG-1998;
 FEATURES Location/Qualifiers
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 source /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
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 Db 2 CAGGCAGC 10

RESULT 201

AR028150

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LOCUS AR028150 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5858660.
ACCESSION AR028150
VERSION AR028150.1 GI:5940123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Eaton,B. and Gold,L.
TITLE Parallel sele
JOURNAL Patent: US 5858660-A 1 12-JAN-1999;
FEATURES
    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 CTGCGACGC 18
Db 2 CAGGCACGC 10
RESULT 202
AR074450/c
LOCUS AR074450 10 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 21 from patent US 5955075.
ACCESSION AR074450
VERSION AR074450.1 GI:10001205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 21 21-SEP-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCT 11
Db 10 GGACTAGCT 2
RESULT 203
AR081130/c
LOCUS AR081130 10 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 21 from patent US 5972353.
ACCESSION AR081130
VERSION AR081130.1 GI:10007858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 5972353-A 21 26-OCT-1999;
FEATURES
    Location/Qualifiers
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            /mol_type="unassigned DNA"
LOCUS AR028150 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5858660.
ACCESSION AR028150
VERSION AR028150.1 GI:5940123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Eaton,B. and Gold,L.
TITLE Parallel sele
JOURNAL Patent: US 5858660-A 1 12-JAN-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 CTGCGACGC 18
Db 2 CAGGCACGC 10
RESULT 202
AR074450/c
LOCUS AR074450 10 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 21 from patent US 5955075.
ACCESSION AR074450
VERSION AR074450.1 GI:10001205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 21 21-SEP-1999;
FEATURES
    Location/Qualifiers
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Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCT 11
Db 10 GGACTAGCT 2
RESULT 203
AR081130/c
LOCUS AR081130 10 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 21 from patent US 5972353.
ACCESSION AR081130
VERSION AR081130.1 GI:10007858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 5972353-A 21 26-OCT-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
LOCUS AR085327/c
LOCUS AR085327 10 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 21 from patent US 5981711.
ACCESSION AR085327
VERSION AR085327.1 GI:10012096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 21 09-NOV-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCT 11
Db 10 GGACTAGCT 2
RESULT 204
AR085327/c
LOCUS AR085327 10 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 21 from patent US 5981711.
ACCESSION AR085327
VERSION AR085327.1 GI:10012096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 21 09-NOV-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCT 11
Db 10 GGACTAGCT 2
RESULT 205
AR088075/c
LOCUS AR088075 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 21 from patent US 5989838.
ACCESSION AR088075
VERSION AR088075.1 GI:10014838
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 21 23-NOV-1999;
FEATURES
    Location/Qualifiers
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGACTCGCT 11
Db 10 GGACTAGCT 2
RESULT 206
AR104234/c
LOCUS AR104234 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6095548.
ACCESSION AR104234
VERSION AR104234.1 GI:12816942
KEYWORDS
SOURCE Unknown.
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PC  C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
GO1N37/00,
CC  C12N15/00,C12N5/00,C12N15/00
CC  Preparation and use of superior vaccines
FH  Key Location/Qualifiers
FT  source 1..10
FT  Location/Qualifiers
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      1..10
      /organism='Homo sapiens'
      /mol_type='genomic DNA'
      /db_xref='taxon:9606'

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TCCTGGCA 15
    |||||
Db 9 TAGCTGGCA 1

RESULT 210
BD239061
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239061
VERSION BD239061.1 GI:33048831
KEYWORDS JP 2002534056-A/479.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 479 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/479
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
      /organism='Homo sapiens (human)'.
      1..10
      /organism='Homo sapiens'
      /mol_type='genomic DNA'
      /db_xref='taxon:9606'

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19
    |||||
Db 2 TGGCAGCA 10

RESULT 212
BD239149/c
LOCUS
DEFINITION Preparation and use of superior vaccines.

```

```

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14
    |||||
Db 2 CTGGCTGGC 10

RESULT 211
BD239128
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239128
VERSION BD239128.1 GI:33048898
KEYWORDS JP 2002534056-A/546.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 546 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/546
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
      /organism='Homo sapiens (human)'.
      1..10
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      /mol_type='genomic DNA'
      /db_xref='taxon:9606'

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19
    |||||
Db 2 TGGCAGCA 10

RESULT 212
BD239149/c
LOCUS
DEFINITION Preparation and use of superior vaccines.

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ACCESSION   BD239149
VERSION     BD239149.1 GI:33048919
KEYWORDS    JP 2002534056-A/567.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 567 15-OCT-2002;
            GENZYME CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2002534056-A/567
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090035 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS, SRINIVAS SHANKARA
            PC C12N15/09,C12N15/03,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            GOIN37/00,
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGCC 14
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Db 10 CTCGCTGCC 2

RESULT 213
BD239806
LOCUS       BD239806
DEFINITION Preparation and use of superior vaccines.
ACCESSION   BD239806
VERSION     BD239806.1 GI:33049576
KEYWORDS    JP 2002534056-A/1224.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 1224 15-OCT-2002;
            GENZYME CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2002534056-A/1224
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
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            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS, SRINIVAS SHANKARA
            PC C12N15/09,C12N15/03,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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            CC Preparation and use of superior vaccines
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGCC 14
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Db 10 CTCGCTGCC 2

RESULT 213
BD239806
LOCUS       BD239806
DEFINITION Preparation and use of superior vaccines.
ACCESSION   BD239806
VERSION     BD239806.1 GI:33049576
KEYWORDS    JP 2002534056-A/1224.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 1224 15-OCT-2002;
            GENZYME CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2002534056-A/1224
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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            08-DEC-1998 US 60/111715
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCA 19
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Db 2 TGGCAGCA 10

RESULT 214
BD270828
LOCUS       BD270828
DEFINITION Parallel selel.
ACCESSION   BD270828
VERSION     BD270828.1 GI:33080596
KEYWORDS    JP 2002526511-A/1.
SOURCE      synthetic construct
            ORGANISM    synthetic construct
            REFERENCE   1 (bases 1 to 10)
            AUTHORS     Eaton,B. and Tarasow,T.M.
            TITLE       Parallel selel
            JOURNAL     Patent: JP 2002526511-A 1 20-AUG-2002;
            INVENUX INC
            COMMENT      OS Artificial Sequence
            OS Unknown
            PN JP 2002526511-A/1
            PD 20-AUG-2002
            PF 13-SEP-1999 JP 2000574297
            PR 21-SEP-1998 US 09/157601
            PI BRUCE EATON, THEODORE M TARASOW
            PC C07H21/00,C07B61/00,C12N15/09,GOIN33/15,GOIN33/50,GOIN33/50//
            PC A61K45/00,
            CC C12N15/00,
            CC artificial DNA sequence
            FH Key Location/Qualifiers
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/organism="Homo sapiens"
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCGC 18
Db 2 CAGGCACGC 10

RESULT 225
AX153207
LOCUS      AX153207      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1122 from Patent WO0138577.
ACCESSION  AX153207
VERSION     AX153207.1 GI:14534858
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Velculescu V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 1122 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 226
AX153311
LOCUS      AX153311      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1226 from Patent WO0138577.
ACCESSION  AX153311
VERSION     AX153311.1 GI:14534962
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 1226 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source          1..10
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 227
AX153312
LOCUS      AX153312      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1227 from Patent WO0138577.
ACCESSION  AX153312
VERSION     AX153312.1 GI:14534963
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 1227 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCGCA 19
Db 2 TGGCAGCGCA 10

RESULT 228
AX153453
LOCUS      AX153453      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1368 from Patent WO0138577.
ACCESSION  AX153453
VERSION     AX153453.1 GI:14535104
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 1368 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCGAC 20
Db 1 GGCAGGCAC 9

RESULT 229
AX302591/c
LOCUS      AX302591      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 109 from Patent WO0175177.
ACCESSION  AX302591
VERSION     AX302591.1 GI:17383118
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE Morin, P. J., Sherman-Baust, C. A., Pizer, E. S. and Hough, C. D.

AUTHORS Tumor markers in ovarian cancer

TITLE Patent: WO 01/75177-A 103 11-OCT-2001;

JOURNAL THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. NO. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCA 19

Db 10 TGGCAGCA 2

RESULT 230

AX469413/c

LOCUS Sequence 4 from Patent WO0233376.

DEFINITION AX469413

ACCESSION AX469413.1 GI:21901709

VERSION

KEYWORDS Hepatitis C virus

SOURCE Hepatitis C virus

ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1

AUTHORS Balakireva, L.

TITLE Polypeptides inhibiting hepatitis c virus internal ribosome entry site (IRES), and method for screening said polypeptides

JOURNAL Patent: WO 0233376-A 4 25-APR-2002;

FEATURES PARTEUROP DEVELOPEMENT (FR)

Location/Qualifiers

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/organism="Hepatitis C virus"

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/db_xref="taxon:11103"

/note="Sequence de la boucle IIIC"

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. NO. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGACGCGC 20

Db 9 GGACGCGC 1

RESULT 231

AX469413/c

LOCUS Sequence 567 from Patent WO0242459.

DEFINITION AX469413

ACCESSION AX469413.1 GI:29291268

VERSION

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Liu, Q.

TITLE Position dependent recognition of gnn nucleotide triplets by zinc

JOURNAL Patent: WO 0242459-A 567 30-MAY-2002;

FEATURES Sangamo Biosciences Inc. (US)

Location/Qualifiers

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="example target DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. NO. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16

Db 9 CGCTGGCAC 1

RESULT 232

AX667119/c

LOCUS Sequence 568 from Patent WO0242459.

DEFINITION AX667119

ACCESSION AX667119.1 GI:29291269

VERSION

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Liu, Q.

TITLE Position dependent recognition of gnn nucleotide triplets by zinc

JOURNAL Patent: WO 0242459-A 568 30-MAY-2002;

FEATURES Sangamo Biosciences Inc. (US)

Location/Qualifiers

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/organism="synthetic construct"

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/note="example target DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. NO. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCTGGCAC 16

Db 9 CGCTGGCAC 1

RESULT 233

BD161317/c

LOCUS Human activated Th1 and Th2 cell expression genes.

DEFINITION BD161317

ACCESSION BD161317.1 GI:27867075

VERSION

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1

AUTHORS Nagai, S., Matsushima, K. and Hashimoto, S.

TITLE Human activated Th1 and Th2 cell expression genes

JOURNAL Patent: JP 2002186482-A 139 02-JUL-2002;

COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002186482-A/139

PD 02-JUL-2002

PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC

CI2N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human

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Location/Qualifiers

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FEATURES Location/Qualifiers

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PI	KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI			
YAMASHITA				
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PC	C12P21/08,			
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CC	Human liver disease-expressing genes			
CC	Human liver disease-expressing genes			
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Db	2	TGGCAGCGCA	10	
RESULT 236				
BD166788				
LOCUS			10 bp	DNA
DEFINITION			Human liver disease-expressing genes.	linear
ACCESSION				
VERSION			BD166788.1	GI:27872600
KEYWORDS			JP 200209591-A/333.	
SOURCE			unidentified	
ORGANISM			unclassified.	
REFERENCE			1 (bases 1 to 10)	
AUTHORS			Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.	
TITLE			Human liver disease-expressing genes	
JOURNAL			Patent: JP 200209591-A 333 30-JUL-2002;	
COMMENT			JAPAN SCIENCE AND TECHNOLOGY CORP	
			OS Homo sapiens (human)	
			PN JP 200209591-A/333	
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PF	19-JAN-2001	JP	2001012328	
PI	KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI			
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PC	C12P21/08,			
PC	C12N15/00,			
CC	Human liver disease-expressing genes			
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			0; Gaps	
QY	3	GGACTCGCT	11	
Db	2	GGACGCGCT	10	
RESULT 237				
BD166869				
LOCUS			10 bp	DNA
DEFINITION			Human liver disease-expressing genes.	linear
ACCESSION				
VERSION			BD166869	
KEYWORDS			unidentified	
SOURCE			unclassified.	
ORGANISM			unclassified.	
REFERENCE			1 (bases 1 to 10)	
AUTHORS			Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.	
TITLE			Human liver disease-expressing genes	
JOURNAL			Patent: JP 200209591-A 333 30-JUL-2002;	
COMMENT			JAPAN SCIENCE AND TECHNOLOGY CORP	
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PI	KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI			
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PC	C12P21/08,			
PC	C12N15/00,			
CC	Human liver disease-expressing genes			
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Query Match			37.0%;	Score 7.4; DB 1; Length 10;
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Matches	8; Conservative		0; Mismatches	1; Indels
			0; Gaps	
QY	3	GGACTCGCT	11	
Db	2	GGACGCGCT	10	
RESULT 237				
BD166869				
LOCUS			10 bp	DNA
DEFINITION				

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VERSION	BD166960.1	GI:27872681			
KEYWORDS	JP 2002209591-A/414.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.				
TITLE	Human liver disease-expressing genes				
JOURNAL	Patent: JP 2002209591-A 414 30-JUL-2002;				
COMMENT	JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2002209591-A/414 PD 30-JUL-2002 PF 19-JAN-2001 JP 2001012328 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI YAMASHITA PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02, PC C12P21/08, PC C12N15/00 CC Human liver disease-expressing genes FH Key Location/Qualifiers FT source 1..10 /location/Qualifiers (human)'.				
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	/db_xref='taxon:32644'				
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Best Local Similarity	88.9%;	Pred. No. 1.1e+02;			
Matches	8; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
Qy	11 TGGCAGGCA 19				
Db	2 TGCACGGCA 10				
RESULT 238					
BD166960					
LOCUS	BD166960	10 bp	DNA	linear	PAT 17-JAN-2003
DEFINITION	Human liver disease-expressing genes.				
ACCESSION	BD166960				
VERSION	BD166960.1	GI:27872772			
KEYWORDS	JP 2002209591-A/505.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.				
TITLE	Human liver disease-expressing genes				
JOURNAL	Patent: JP 2002209591-A 505 30-JUL-2002;				
COMMENT	JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2002209591-A/505 PD 30-JUL-2002 PF 19-JAN-2001 JP 2001012328 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI YAMASHITA PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02, PC C12P21/08, PC C12N15/00 CC Human liver disease-expressing genes FH Key Location/Qualifiers FT source 1..10 /location/Qualifiers (human)'.				
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source	1..10				
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Query Match	37.0%;	Score 7.4;	DB 1;	Length 10;	


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PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCGCTG 12
    ||| |||||
Db 2 GACGCGCTG 10

RESULT 241
LOCUS BD167055 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167055
VERSION BD167055.1 GI:27872867
KEYWORDS JP 2002209591-A/600.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 600 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/600
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
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        Location/Qualifiers
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            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19
    ||||| |||
Db 10 TGGCAAGCA 2

RESULT 243
LOCUS AR301508 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 89 from patent US 6538173.
ACCESSION AR301508
VERSION AR301508.1 GI:31689310
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 89 25-MAR-2003;
JOURNAL JOURNAL
FEATURES
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        Location/Qualifiers
            1..11
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTCGCTGG 13
    ||| |||||
Db 1 ACTGCTGG 9

RESULT 244
LOCUS AR301596/c 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 177 from patent US 6538173.
ACCESSION AR301596
VERSION AR301596.1 GI:31689398
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)

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AUTHORS Heber-Katz, E.
 TITLE Compositions and methods for wound healing
 JOURNAL Patent: US 638173-A 177 25-MAR-2003;
 FEATURES Location/Qualifiers
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 1..11
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
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 Db 11 ACTGGCTGG 3

RESULT 245
 AX339216/c
 LOCUS AX339216 11 bp DNA linear PAT 10-JAN-2002
 DEFINITION Sequence 10 from Patent WO0196602.
 ACCESSION AX339216
 VERSION AX339216.1 GI:18135477
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Yang, A.L. and Festing, M.
 TITLE Methods and materials to determine the p53 status of a sample by
 determining the binding of p53 to a vector
 JOURNAL Patent: WO 0196602-A 10 20-DEC-2001;
 MEDICAL RESEARCH COUNCIL (GB)

FEATURES Location/Qualifiers
 source
 1..11
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="pGL3-Basic vector"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCG 18
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 Db 11 CTAGCAGCG 3

RESULT 246
 AX393079
 LOCUS AX393079 11 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 9 from Patent WO0210217.
 ACCESSION AX393079
 VERSION AX393079.1 GI:19701129
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL St Croix, B., Kinzler, K.W. and Vogelstein, B.
 Endothelial cell expression patterns
 Patent: WO 0210217-A 9 07-FEB-2002;
 The Johns Hopkins University (US)

FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TCCTCGCA 15
 |||||
 Db 1 TCCTCGCA 9

RESULT 247
 AX470499
 LOCUS AX470499 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 76 from Patent WO02053773.
 ACCESSION AX470499
 VERSION AX470499.1 GI:22205624
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL Hofmann, K., Conradt, M. and Petersohn, D.
 Method for determining skin stress or skin ageing in vitro
 Patent: WO 02053773-A 76 11-JUL-2002;
 HENKEL KGAA (DE)

FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGCG 18
 |||||
 Db 2 CAGGCAGCG 10

RESULT 248
 AX471362
 LOCUS AX471362 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 939 from Patent WO02053773.
 ACCESSION AX471362
 VERSION AX471362.1 GI:22206487
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL Hofmann, K., Conradt, M. and Petersohn, D.
 Method for determining skin stress or skin ageing in vitro
 Patent: WO 02053773-A 939 11-JUL-2002;
 HENKEL KGAA (DE)

FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 37.0%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CTCGCTGGC 14
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 Db 2 CTGGCTGGC 10

RESULT 249
 AX471759/c
 LOCUS AX471759 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 1336 from Patent WO02053773.

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ACCESSION AX471759
VERSION AX471759.1 GI:22206884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1336 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CGCTGGCAC 16
Db 10 CACTGGCAC 2
RESULT 250
AX471838
LOCUS AX471838 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1415 from Patent WO02053773.
ACCESSION AX471838
VERSION AX471838.1 GI:22206963
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1415 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CGCTGGCAC 16
Db 10 CACTGGCAC 2
RESULT 251
AX623182/c
LOCUS AX623182 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 223 from Patent WO02053774.
ACCESSION AX623182
VERSION AX623182.1 GI:28451123
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 223 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)

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FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
Henkel Kommanditgesellschaft auf Aktien (DE)
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACTCGCTGG 13
Db 9 ACTAGCTGG 1
RESULT 252
AX623576
LOCUS AX623576 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 617 from Patent WO02053774.
ACCESSION AX623576
VERSION AX623576.1 GI:28451517
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 617 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GGCACGCAC 20
Db 3 GGCACGCAC 11
RESULT 253
AX623956
LOCUS AX623956 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 997 from Patent WO02053774.
ACCESSION AX623956
VERSION AX623956.1 GI:28451897
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 997 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GGCACGCAC 20
Db 3 GGCACGCAC 11
RESULT 254
AX623956
LOCUS AX623956 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 997 from Patent WO02053774.
ACCESSION AX623956
VERSION AX623956.1 GI:28451897
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 997 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GGCACGCAC 20
Db 3 GGCACGCAC 11

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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CTGGCAGC 18
Db 2 CAGGCAGC 10

RESULT 259
AX627150/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4191 from Patent WO02053774.
ACCESSION  AX627150
VERSION     AX627150.1 GI:28455188
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 4191 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGTGGCAGC 16
Db 10 CTCTGGCAGC 2

RESULT 260
AX628244
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5285 from Patent WO02053774.
ACCESSION  AX628244
VERSION     AX628244.1 GI:28456282
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5285 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCGCTGSCA 15
Db 11

RESULT 261
AX628489/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5530 from Patent WO02053774.
ACCESSION  AX628489
VERSION     AX628489.1 GI:28456527
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5530 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCAGCAGCA 19
Db 9 TGGCAGCAGCA 1

RESULT 262
AX628643/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5684 from Patent WO02053774.
ACCESSION  AX628643
VERSION     AX628643.1 GI:28456681
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5684 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCACGCAC 20
Db 11 GGCACCCAC 3

RESULT 263
AX629283
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6324 from Patent WO02053774.
ACCESSION  AX629283
VERSION     AX629283.1 GI:28457321
KEYWORDS
SOURCE      Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 6324 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.0%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GACTCTCTG 12
    |||||
Db 1 GACTCTCTG 9

RESULT 264
AX629630
LOCUS AX629630 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6671 from Patent WO02053774.
ACCESSION AX629630
VERSION AX629630.1 GI:28457668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 6671 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  Location/Qualifiers
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.0%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGACTCG 9
    |||||
Db 2 ACGGACTCG 10

RESULT 265
AX629833
LOCUS AX629833 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6874 from Patent WO02053774.
ACCESSION AX629833
VERSION AX629833.1 GI:28457871
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 6874 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  Location/Qualifiers
  source
    1..11
    /organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.0%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCAGCA 19
    |||||
Db 2 TGGCAGCA 10

RESULT 266
AX629906
LOCUS AX629906 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6947 from Patent WO02053774.
ACCESSION AX629906
VERSION AX629906.1 GI:28457944
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 6947 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  Location/Qualifiers
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.0%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GGCAGGCAC 20
    |||||
Db 1 GGCAGGCAC 9

RESULT 267
AX630246
LOCUS AX630246 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7287 from Patent WO02053774.
ACCESSION AX630246
VERSION AX630246.1 GI:28458284
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 7287 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  Location/Qualifiers
  source
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.0%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCGCTGGC 14
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Db 2 CTCGCTGGC 10

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RESULT 269
AX630603/c
LOCUS      AX630603      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7644 from Patent WO02053774.
ACCESSION  AX630603
VERSION     AX630603.1 GI:28458641
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7644 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ACTCGCTGG 13
        |||||
Db      9 ACTAGCTGG 1

RESULT 269
AX630997
LOCUS      AX630997      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8038 from Patent WO02053774.
ACCESSION  AX630997
VERSION     AX630997.1 GI:28459039
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8038 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GGCACGCAC 20
        |||||
Db      3 GGCACACAC 11

RESULT 270
AX631377
LOCUS      AX631377      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8419 from Patent WO02053774.
ACCESSION  AX631377
VERSION     AX631377.1 GI:28459443
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8419 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CTGGCAGCC 18
        |||||
Db      1 CTGGCAGCC 9

RESULT 271
AX631802/c
LOCUS      AX631802      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8844 from Patent WO02053774.
ACCESSION  AX631802
VERSION     AX631802.1 GI:28459909
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8844 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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               /mol_type="unassigned DNA"
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Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GGCACGCAC 20
        |||||
Db      9 GGCACCTCAC 1

RESULT 272
AX632450/c
LOCUS      AX632450      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9492 from Patent WO02053774.
ACCESSION  AX632450
VERSION     AX632450.1 GI:28468065
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 9492 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

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Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGACTGCG 10
DB 9 TGGACTGCG 1

RESULT 273
BD124258
LOCUS      11 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION  BD124258
VERSION     BD124258.1 GI:23219203
KEYWORDS    JP 2002503460-A/89.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 11)
AUTHORS     Katz,E.H.
TITLE       Compositions and method for healing wound
JOURNAL     THE WISTAR INSTITUTE
COMMENT     OS Mus musculus (mouse)
            PN JP 2002503460-A/89
            PD 05-FEB-2002
            PR 12-FEB-1999 JP 2000531545
            PF 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
            PI ELLEN HEBER KATZ
            PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,GO1N33/50,C12N15/00,PC
            C12N5/00
            CC Compositions and method for healing wound
            FH Key Location/Qualifiers
            FT source 1.11
              /organism='Mus musculus (mouse)'.

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
DB 1 ACTGGCTGG 9

RESULT 274
BD124346/c
LOCUS      11 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION  BD124346
VERSION     BD124346.1 GI:23219291
KEYWORDS    JP 2002503460-A/177.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 11)
AUTHORS     Katz,E.H.
TITLE       Compositions and method for healing wound
JOURNAL     THE WISTAR INSTITUTE
COMMENT     OS Mus musculus (mouse)
            PN JP 2002503460-A/177
            PD 05-FEB-2002
            PR 12-FEB-1999 JP 2000531545
            PF 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
            PI ELLEN HEBER KATZ
            PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,GO1N33/50,C12N15/00,PC
            C12N5/00
            CC Compositions and method for healing wound
            FH Key Location/Qualifiers
            FT source 1.11
              /organism='Mus musculus (mouse)'.

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
DB 1 ACTGGCTGG 9

RESULT 275
BD124346/c
LOCUS      11 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168870.
ACCESSION  AX250557
VERSION     AX250557.1 GI:15984293
KEYWORDS    synthetic construct
            artificial construct
            sequences
            1 (bases 1 to 9)
            HANSON,A.D., Nuccio,M.L. and Henry,S.A.
            S-adenosyl-L-methionine:phosphoethanolamine n-methyltransferase
            compositions and methods for modulating lipid biosynthesis in
            plants
            Patent: WO 0168870-A 7 20-SEP-2001;
            University of Florida (US); Carnegie-Mellon University (US)
            Location/Qualifiers
            FT source 1.9
              /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
              /note='SYNTHETIC OLIGONUCLEOTIDE'

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
DB 9 TGGCAGC 3

RESULT 276
AX456625
LOCUS      9 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 97 from Patent WO0218407.
ACCESSION  AX456625
VERSION     AX456625.1 GI:21715512
KEYWORDS    Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1
AUTHORS     Kurreck,J. and Erdmann,V.A.
TITLE       Antisense oligonucleotides against vrl

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
DB 9 TGGCAGC 3

RESULT 277
AX456625
LOCUS      9 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 97 from Patent WO0218407.
ACCESSION  AX456625
VERSION     AX456625.1 GI:21715512
KEYWORDS    Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1
AUTHORS     Kurreck,J. and Erdmann,V.A.
TITLE       Antisense oligonucleotides against vrl

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PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,GO1N33/50,C12N15/00,PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1.11
  /organism='Mus musculus (mouse)'.

Query Match      37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTCGCTGG 13
DB 11 ACTGGCTGG 3

RESULT 275
AX250557/c
LOCUS      9 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168870.
ACCESSION  AX250557
VERSION     AX250557.1 GI:15984293
KEYWORDS    synthetic construct
            artificial construct
            sequences
            1 (bases 1 to 9)
            HANSON,A.D., Nuccio,M.L. and Henry,S.A.
            S-adenosyl-L-methionine:phosphoethanolamine n-methyltransferase
            compositions and methods for modulating lipid biosynthesis in
            plants
            Patent: WO 0168870-A 7 20-SEP-2001;
            University of Florida (US); Carnegie-Mellon University (US)
            Location/Qualifiers
            FT source 1.9
              /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
              /note='SYNTHETIC OLIGONUCLEOTIDE'

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
DB 9 TGGCAGC 3

RESULT 276
AX456625
LOCUS      9 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 97 from Patent WO0218407.
ACCESSION  AX456625
VERSION     AX456625.1 GI:21715512
KEYWORDS    Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1
AUTHORS     Kurreck,J. and Erdmann,V.A.
TITLE       Antisense oligonucleotides against vrl

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JOURNAL      Patent: WO 0218407-A 97 07-MAR-2002;
FEATURES      Gruenenthal GmbH (DE)
source        Location/Qualifiers
1..9
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTC 8
Db 2 TGGACTC 8

RESULT 277
AX456642
LOCUS      AX456642      9 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION      Sequence 114 from Patent WO0218407.
ACCESSION      AX456642
VERSION      AX456642.1 GI:21715529
KEYWORDS
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1
AUTHORS      Kurreck, J. and Erdmann, V. A.
TITLE      Antisense oligonucleotides against vrl
JOURNAL      Patent: WO 0218407-A 114 07-MAR-2002;
Gruenenthal GmbH (DE)
FEATURES      Location/Qualifiers
source        1..9
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTC 8
Db 2 TGGACTC 8

RESULT 278
AX668929
LOCUS      AX668929      9 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION      Sequence 2378 from Patent WO0242459.
ACCESSION      AX668929
VERSION      AX668929.1 GI:29291906
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Liu, Q.
TITLE      Position dependent recognition of gun nucleotide triplets by zinc
JOURNAL      Patent: WO 0242459-A 2378 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES      Location/Qualifiers
source        1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="example target DNA"

Query Match      35.0%; Score 7; DB 1; Length 9;

JOURNAL      Patent: WO 0218407-A 97 07-MAR-2002;
FEATURES      Gruenenthal GmbH (DE)
source        Location/Qualifiers
1..9
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACTC 8
Db 2 TGGACTC 8

RESULT 279
S81508/c
LOCUS      S81508      9 bp      DNA      linear      PRI 07-MAY-1993
DEFINITION      uroporphyrinogen III synthase [human, Genomic Mutant, 9 nt].
ACCESSION      S81508
VERSION      S81508.1 GI:245377
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 9)
AUTHORS      Warner, C. A., Yoo, H. W., Roberts, A. G. and Desnick, R. J.
TITLE      Congenital erythropoietic porphyria: identification and expression
of exonic mutations in the uroporphyrinogen III synthase gene
JOURNAL      J. Clin. Invest. 89 (2), 693-700 (1992)
MEDLINE      92147890
PubMed      1737856
REMARK      Genbank staff at the National Library of Medicine created this
entry [NCBI gibbsq 81508] from the original journal article.
This sequence comes from Figure 3.
COMMENT      A to G transition nt 184, Thr to Ala replacement residue 62.
FEATURES      Location/Qualifiers
source        1..9
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..9
/gene="uroporphyrinogen III synthase"

Query Match      35.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCA 15
Db 9 GCTGGCA 3

RESULT 280
AR167219/c
LOCUS      AR167219      10 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION      Sequence 53 from patent US 6284466.
ACCESSION      AR167219
VERSION      AR167219.1 GI:16243731
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Benson, A.
TITLE      Method of detecting genetic polymorphisms using over represented
sequences
JOURNAL      Patent: US 6284466-A 53 04-SEP-2001;
Location/Qualifiers
source        1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCTGGC 14
Db 8 CGCTGGC 14

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Db

10 CCGTGC 4

RESULT 281
BD238649
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238649.1 GI:33048419
VERSION JP 2002534056-A/67.
KEYWORDS Homo sapiens (human)
SOURCE GENZYME CORP
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 67 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/71
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
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PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACGCAC 20
DB 9 CACGCAC 3

RESULT 283
BD238676
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238676
VERSION BD238676.1 GI:33048446
KEYWORDS JP 2002534056-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 94 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/94
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
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08-DEC-1998 US 60/111715
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PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCTGG 13
DB 3 TCGCTGG 9

RESULT 282
BD238653/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238653
VERSION BD238653.1 GI:33048423
KEYWORDS JP 2002534056-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 71 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/71
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
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C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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QY 7 TCGCTGG 13
DB 3 TCGCTGG 9

RESULT 283
BD238676
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238676
VERSION BD238676.1 GI:33048446
KEYWORDS JP 2002534056-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 94 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/94
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19

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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACGCAC 20
Db 3 CACGCAC 9

RESULT 284
BD238708 10 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238708.1 GI:33048478
VERSION JP 2002534056-A/126.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 126 15-OCT-2002;
  GENZYME CORP
COMMENT
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  PN JP 2002534056-A/126
  PD 15-OCT-2002
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  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACGCAC 20
Db 3 CACGCAC 9

RESULT 285
BD239100 10 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239100
VERSION BD239100.1 GI:33048870
KEYWORDS JP 2002534056-A/518.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 518 15-OCT-2002;
  GENZYME CORP
COMMENT
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  PN JP 2002534056-A/518
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACGCAC 20
Db 2 CACGCAC 8

RESULT 286
BD239100 10 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239100
VERSION BD239100.1 GI:33048870
KEYWORDS JP 2002534056-A/518.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 518 15-OCT-2002;
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COMMENT
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  PN JP 2002534056-A/518
  PD 15-OCT-2002
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
DB 2 TGGCAGC 8

RESULT 286
LOCUS BD239504 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239504
VERSION BD239504.1 GI:33049274
KEYWORDS JP 2002534056-A/922.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 922 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/922
PD 15-OCT-2002
PF 18-JUN-1998 JP 200554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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QY 14 CAGCAC 20
DB 2 CAGCAC 8

RESULT 287
LOCUS BD239567 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239567
VERSION BD239567.1 GI:33049337
KEYWORDS JP 2002534056-A/985.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 985 15-OCT-2002;

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Dd	3 GACTCGC 9	
RESULT 290		
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LOCUS	BD240040 10 bp DNA linear PAT 17-JUL-2003	
DEFINITION	Preparation and use of superior vaccines.	
ACCESSION	BD240040	
VERSION	BD240040.1 GI:33049810	
KEYWORDS	JP 2002534056-A/1458	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	1 (bases 1 to 10)	
JOURNAL	Roberts,B.L. and Shankara,S.	
COMMENT	Preparation and use of superior vaccines	
	Patent: JP 2002534056-A 1458 15-OCT-2002;	
	GENZYME CORP	
	OS Homo sapiens (human)	
	FN JP 2002534056-A/1458	
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QY 8 CGCTGGC 14
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 Db 10 CGCTGGC 4

RESULT 291

BD240550
 LOCUS 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240550
 VERSION BD240550.1 GI:33050320
 KEYWORDS JP 2002534056-A/1968.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 10)
 AUTHORS Roberts,B.L. and Shankara,S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1968 15-OCT-2002;
 GENZYME CORP

COMMENT

OS Homo sapiens (human)
 PN JP 2002534056-A/1968
 PD 15-OCT-2002

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 19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
 19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
 19-JUN-1998 US 60/089894,19-JUN-1998 US 60/090077 PR
 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
 PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
 C12N1/19

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/565, PC
 G01N37/00,
 PC C12N15/00,C12N5/00,C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
 FT source 1..10
 FT /organism='Homo sapiens (human)'

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source
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 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGCA 15
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 Db 3 GCTGGCA 9

RESULT 292

B39743
 LOCUS 10 bp DNA linear PAT 31-JAN-2002
 DEFINITION Genes with human dendritic cell expression.
 ACCESSION E39743
 VERSION E39743.1 GI:18621834
 KEYWORDS JP 2000279181-A/276.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 10)
 AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
 TITLE Genes with human dendritic cell expression
 JOURNAL Patent: JP 2000279181-A 276 10-OCT-2000;
 SCIENCE & TECH AGENCY

COMMENT

OS Homo sapiens (human)
 PN JP 2000279181-A/276
 PD 10-OCT-2000
 PF 01-APR-1999 JP 1999095481

PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
 C12N15/09,C07K14/475,C07K16/18,C12N15/00

CC Key Location/Qualifiers
 FH source 1..10
 FT Location/Qualifiers
 FT /organism='Homo sapiens (human)'

FEATURES

source
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 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGGCAC 16
 |||||
 Db 4 CTGGCAC 10

RESULT 293

AR222988
 LOCUS 10 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 41 from patent US 6432640.
 ACCESSION AR222988
 VERSION AR222988.1 GI:23330826
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE

1 (bases 1 to 10)
 AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.
 TITLE p53-induced apoptosis
 JOURNAL Patent: US 6432640-A 41 13-AUG-2002;
 LOCATION/Qualifiers

FEATURES

source
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 Location/Qualifiers
 /organism='unknown'
 /mol_type='genomic DNA'

Query Match 35.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTCGC 10
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Db	1	GACTCGC	7
 RESULT 294			
AR241894/c	AR241894		PAT 20-DEC-2002
LOCUS	Sequence 182 from patent US 6472154.	10 bp	DNA linear
DEFINITION			
ACCESSION	AR241894		
VERSION	AR241894.1 GI:27287706		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 10)		
TITLE	Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.		
JOURNAL	Polymorphic repeats in human genes		
FEATURES	Patent: US 6472154-A 182 29-OCT-2002;		
source	Location/Qualifiers		
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	/mol_type="genomic DNA"		
Query Match	35.0%; Score 7; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred.No.1.4e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	14 CACGCAC 20		
Db	10 CACGCAC 4		
 RESULT 295			
AR336858/c	AR336858		PAT 17-AUG-2003
LOCUS	Sequence 33 from patent US 6566130.	10 bp	DNA linear
DEFINITION			
ACCESSION	AR336858		
VERSION	AR336858.1 GI:33722708		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 10)		
TITLE	Strivastava,S., Moull,J.W., Xu,L.L. and Segawa,T.		
JOURNAL	Androgen-regulated gene expressed in prostate tissue		
FEATURES	Patent: US 6566130-A 33 20-MAY-2003;		
source	Location/Qualifiers		
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	/mol_type="genomic DNA"		
Query Match	35.0%; Score 7; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred.No.1.4e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	14 CACGCAC 20		
Db	10 CACGCAC 4		
 RESULT 296			
AX062271	AX062271		PAT 24-JAN-2001
LOCUS	Sequence 130 from Patent WO0100849.	10 bp	DNA linear
DEFINITION			
ACCESSION	AX062271		
VERSION	AX062271.1 GI:12540172		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
	Christenson,E., Demaggio,A.J., Goldman,P.S. and Mcelligott,D.L.		
	Tankyrase2 materials and methods		

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Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TGGACTC 8
    |||||
Db   8 TGGACTC 2

RESULT 299
AX152322
LOCUS      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 237 from Patent WO0138577.
ACCESSION  AX152322
VERSION     AX152322.1 GI:14533973
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 237 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 CGCTGGC 14
    |||||
Db   3 CGCTGGC 9

RESULT 300
AX152374
LOCUS      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 289 from Patent WO0138577.
ACCESSION  AX152374
VERSION     AX152374.1 GI:14534025
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 289 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  14 CACGCAC 20
    |||||
Db   3 CACGCAC 9

RESULT 301
AX152532/c
LOCUS      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 447 from Patent WO0138577.

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ACCESSION  AX152532
VERSION     AX152532.1 GI:14534183
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 447 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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            1..10
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 TCGCTGG 13
    |||||
Db   10 TCGCTGG 4

RESULT 302
AX152540/c
LOCUS      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 455 from Patent WO0138577.
ACCESSION  AX152540
VERSION     AX152540.1 GI:14534191
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 455 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 TGGCAGC 17
    |||||
Db   10 TGGCAGC 4

RESULT 303
AX152750/c
LOCUS      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 665 from Patent WO0138577.
ACCESSION  AX152750
VERSION     AX152750.1 GI:14534401
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 665 31-MAY-2001;

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FEATURES
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      1. .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 35.0%; Score 7; DB 1; Length 10;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACGCAC 20
Db 10 CACGCAC 4

RESULT 304
AX152958
LOCUS AX152958 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 873 from Patent WO0138577.
ACCESSION AX152958
VERSION AX152958.1 GI:14534609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 873 31-MAY-2001;
  The Johns Hopkins University (US)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 35.0%; Score 7; DB 1; Length 10;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCCTCG 13
Db 3 TCCTCG 9

RESULT 305
AX153036
LOCUS AX153036 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 951 from Patent WO0138577.
ACCESSION AX153036
VERSION AX153036.1 GI:14534687
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 951 31-MAY-2001;
  The Johns Hopkins University (US)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 35.0%; Score 7; DB 1; Length 10;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACGCAC 20
Db 10 CACGCAC 4

RESULT 306
AX153231/c
LOCUS AX153231 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1146 from Patent WO0138577.
ACCESSION AX153231
VERSION AX153231.1 GI:14534882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
  1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1146 31-MAY-2001;
  The Johns Hopkins University (US)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 35.0%; Score 7; DB 1; Length 10;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCACGCA 19
Db 10 GCACGCA 4

RESULT 307
AX302580/c
LOCUS AX302580 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 98 from Patent WO0175177.
ACCESSION AX302580
VERSION AX302580.1 GI:17383107
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Morin,P.J., Sherman-Baust,C.A., Pizer,B.S. and Hough,C.D.
  Tumor markers in ovarian cancer
  Patent: WO 0175177-A 98 11-OCT-2001;
  THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
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    Location/Qualifiers
      1. .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 35.0%; Score 7; DB 1; Length 10;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACGCAC 20
Db 10 CACGCAC 4

RESULT 308
AX374638
LOCUS AX374638 10 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 59 from Patent WO0210454.
ACCESSION AX374638
VERSION AX374638.1 GI:19169535

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KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS Choi,J.Y., Koshy,B., Klem,S. and Stephens,J.C.
TITLE Haplotypes of the alas2 gene
JOURNAL Patent: WO 0210454-A 59 07-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTGGCAC 16
Db 1 CTGGCAC 7
RESULT 309
AX472090
LOCUS AX472090 10 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 81 from Patent WO02053775.
ACCESSION AX472090
VERSION AX472090.1 GI:22207131
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Huxtert,E., Haberl,M. and Wojnowski,L.
TITLE Identification of the genetic determinants of the polymorphic
JOURNAL cyp3a5 expression
Patent: WO 02053775-A 81 11-JUL-2002;
EPIDAURS BIOTECHNOLOGIE AG (DE)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACT 7
Db 2 ATGGACT 8
RESULT 310
BD007979
LOCUS BD007979 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007979
VERSION BD007979.1 GI:18636352
KEYWORDS JP 2001069993-A/255.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 255 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/255
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key 1. .10 Location/Qualifiers
FT source /organism="Homo sapiens (human)".
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTGGCAC 16
Db 4 CTGGCAC 10
RESULT 311
BD008019
LOCUS BD008019 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD008019
VERSION BD008019.1 GI:18636392
KEYWORDS JP 2001069993-A/295.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 295 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/295
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
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FH Key 1. .10 Location/Qualifiers
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 TCGCTGG 13
Db 3 TCGCTGG 9
RESULT 312

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BD091163
LOCUS BD091163 10 bp DNA linear PAT 27-AUG-2002
DEFINITION P53-induced apoptosis.
ACCESSION BD091163
VERSION BD091163.1 GI:22636773
KEYWORDS JP 2001523441-A/41.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE P53-induced apoptosis
JOURNAL THE JOHNS HOPKINS UNIVERSITY
COMMENT OS Homo sapiens (human)
PN JP 2001523441-A/41
PD 27-NOV-2001
PF 17-SEP-1998 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
apoptosis
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GACTCGC 10
Db 1 GACTCGC 7
RESULT 313
BD143088
LOCUS BD143088 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for discriminating the sex of papaya using DNA marker.
ACCESSION BD143088
VERSION BD143088.1 GI:27848846
KEYWORDS JP 2002112773-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Tokumoto,M., Urasaki,N. and Terauchi,R.
TITLE Method for discriminating the sex of papaya using DNA marker
JOURNAL OKINAWA PREF
COMMENT OS Artificial Sequence
PN JP 2002112773-A/3
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303268
PI MASAKAZU TOKUMOTO,NAOYA URASAKI,RYOHEI TERAUCHI PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence:synthetic DNA FH Key
Location/Qualifiers
FT source 1..10
/organism='Artificial Sequence'.
FEATURES
source
1..10
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 35.0%; Score 7; DB 1; Length 10;

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TGGCAGC 17
Db 2 TGGCAGC 8
RESULT 314
BD166515
LOCUS BD166515 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166515
VERSION BD166515.1 GI:27872327
KEYWORDS JP 2002209591-A/60.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
AUTHORS Human liver disease-expressing genes
TITLE Patent: JP 2002209591-A 60 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/60
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
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1..10
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
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QY 14 CACGCAC 20
Db 10 CACGCAC 4
RESULT 315
BD166632
LOCUS BD166632 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166632
VERSION BD166632.1 GI:27872444
KEYWORDS JP 2002209591-A/177.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
AUTHORS Human liver disease-expressing genes
TITLE Patent: JP 2002209591-A 177 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/177
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,

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PC C12P21/08,
CC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCAGC 17
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Db 2 TGGCAGC 8

RESULT 316
BD166724/c
LOCUS 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166724
VERSION BD166724.1 GI:27872536
KEYWORDS JP 2002209591-A/269.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 269 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/269
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
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            /db_xref="taxon:32644"
Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CAGCAC 20
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Db 10 CAGCAC 4

RESULT 317
BD168603/c
LOCUS 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Medicinal compositions for promoting recovery from stress-loading
and novel matsutake mushroom strain.
ACCESSION BD168603
VERSION BD168603.1 GI:27874415
KEYWORDS WO 0230440-A/4.
SOURCE synthetic construct

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ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 10)
REFERENCE Matsunaga,K.
AUTHORS Medicinal compositions for promoting recovery from stress-loading
TITLE and novel matsutake mushroom strain
JOURNAL Patent: WO 0230440-A 4 18-APR-2002;
COMMENT KUREHA CHEMICAL INDUSTRY CO LTD, KENICHI MATSUNAGA
OS Artificial Sequence
PN WO 0230440-A/4
PD 18-APR-2002
PF 10-OCT-2001 WO 2001JP008876
PR 11-OCT-2000 JP COP 311034, 11-OCT-2000 JP OOP 311035 PI
KENICHI MATSUNAGA
PC A61K35/84, A61K7/26, A61P3/00, A23L1/28, A23L1/29, C12N1/14 CC
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Query Match 35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCACGCA 19
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Db 7 GCACGCA 1

RESULT 318
BD234977/c
LOCUS 12 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234977
VERSION BD234977.1 GI:33044747
KEYWORDS JP 2002517434-A/81.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 81 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/81
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
BRYSCH
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/
PC 00, A61P35/00,
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Homo sapiens (human)'.
FEATURES
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        Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match 35.0%; Score 7; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 GACTCGC 10
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Db 7 GACTCGC 1

Search completed: June 8, 2004, 12:21:51
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